

Db 331 KGRVQRPFLPLPELCTRKSHGGQDGGRODYHSGJCS 339

RESULT 2

C5897

Killer cell inhibitory receptor p31 precursor - human

C1Species: Homo sapiens (man)

C1Date: 16-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999

C1Accession: J05897

C1Yamashita, Y.; Fukui, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohya

C1Biochem. 123, 358-368, 1998

C1Title: Genomic structures and chromosomal location of p31, a novel murine regulatory

C1Reference number: J05894; MIMD:98218758; PMID:9538215

C1Accession: J05897

C1Status: Nucleic acid sequence not shown

C1Molecule type: mRNA

C1Residues: 1-466 <YAY>

C1Cross-references: GB:AF04.034; NID:9270.688; P1DN:AB596826.1; P1D:92701690

C1Comment: This protein function as inhibitory cell-surface molecule against cell activa

C1Genetics: A:Map position: 19q13.3-13.4

C1Xref position: signal sequence #status predicted <SIG>

C1Xref position: signal sequence #status predicted <SIG>

C1Xref position: signal sequence #status predicted <SIG>

C1Xref position: signal sequence #status predicted <SIG>

C1Xref position: signal sequence #status predicted <SIG>

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C1Xref position: signal sequence #status predicted <SIG>

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C1Xref position: signal sequence #status predicted <SIG>

C1Xref position: signal sequence #status predicted <SIG>

C1Xref position: signal sequence #status predicted <SIG>

C1Xref position: signal sequence #status predicted <SIG>

C1Xref position: signal sequence #status predicted <SIG>

QY 1 MSPPTALFCLGCLG-RVPAQSGPLPKPS-DALPSS-VPLKPYTRCCGPGVDLYRL 59

Db 1 NAPTLPALCLGCLGCLG-RVPAQSGPLPKPS-DALPSS-VPLKPYTRCCGPGVDLYRL 60

QY 60 EKLSSS-----RCCQAVLFLPAKRS-LAGYRCGNGS-WSLPSQCLEVATG- 109

Db 61 NKEGDTNPNHPS-LEPDKAFPLSNR3QAGVHCSHFGVNMSPSEPEPLVAGE 120

QY 110 -----VFAKPS-LAQPQPAVSSGGDVT-CCQTRVCFDQFALYKES--DFAFYKNPER- 159

Db 121 EPAGLRBPPLSVSPSPVAVAGENVTL-LLCCSNKRTDPLLSKEGAARPLRLSQDDG 180

QY 160 WPAAPPTLVTAAGSGYRCYFSSSDPYLWSASDFLELVYVTSITPSKLFTEPPSS 219

Db 181 WYQAFSS-SPVTAAGCYRCYRSLSTPPLLSGSEPLALVAD----- 225

QY 220 VAEFSPATLVLVSTNKKVFTETSRSTITSTKEGSDSAGPARQYTKGLVRCGAVI 279

Db 226 -----YTCNLIIRNGLASV 240

QY 240 LILAGFLAEQWHSRKRRLRHRGRAVGRPPLPLPOTRKSHG 324

Db 241 LLL-LGL-----LCCQRHDSG 257

RESULT 4

CH0332

1GA (Fc) receptor, myeloid cell (CD89) precursor - human

C1Alternate names: myeloid 5-glycoprotein CD89

C1Species: Homo sapiens (man)

C1Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999

C1Accession: JH0332; J17224; S14435

C1Yalaszewski, C.R.; March, C.C.; Schoenborn, Y.A.; Gimpe, S.; Shen, L.

C1Exp. Med. 172, 1665-1672, 1993

C1Title: Expression cloning of a human Fc receptor for 1GA.

C1Reference number: CH0332; MIMD:91079769; PMID:1225898

C1Accession: JH0332

C1Molecule type: mRNA

C1Residues: 1-287 <MAL>

C1Cross-references: GB:K54150; NID:931229; P1DN:CAA8089.1; P1D:931330

C1Experimental source: myeloid cell liver V937

C1S:de Wit, T.F.; Morton, H.C.; Capel, P.D.; van de Winkel, J.G.

C1Immunol. 155, 1203-1209, 1995

C1Title: Structure of the gene for the human myeloid 1GA Fc receptor (CD89).

C1Reference number: 137224; MIMD:95363085; PMID:7636188

C1Accession: J17224

C1Status: preliminary; translated from GB/EXBL/DBJ

C1Molecule type: DNA

C1Cross-references: EXBL:887767; NID:9963641; P1DN:CAA61039.1; P1D:91054737

C1Genetics:

A:Gene: GDB:FCAR; CD89

A:Cross-references: GDB:127543; OMIM:147045

A:Map position: 19q13.2-19q13.4

A:Introns: 12/1; 24/1; 121/1; 27/1

C1Keywords: glycoprotein; immunoglobulin receptor; transmembrane protein

F:121/Domain: signal sequence status predicted <SIG>

F:22-287/Product: 1GA receptor Fc alpha 1 status predicted <MFC>

F:228-246/Domain: transmembrane status predicted <TMA>

F:65,75,141,177,186/Binding site: carbohydrate (asn) (covalent) status predicted

Query Match 21.9%; Score 397; DB 2; Length 287;

Best Local Similarity 31.2%; Pred. No. 2.3e-21;

Matches 100; Conservative 43; Xismatches 110; Indels 68; Gaps 5;

QY 1 MSPPTALFCLGCLG-RVPAQSGPLPKPS-DALPSS-VPLKPYTRCCGPGVDLYRL 59

Db 1 NAPTLPALCLGCLGCLG-RVPAQSGPLPKPS-DALPSS-VPLKPYTRCCGPGVDLYRL 60

QY 60 EKLSSSRYD-----QAVLFPAKRS-LAGYRCGNGS-WSLPSQCLEVATG- 108

Db 61 NKEGDTNPNHPS-LEPDKAFPLSNR3QAGVHCSHFGVNMSPSEPEPLVAGE 120

QY 110 -----VFAKPS-LAQPQPAVSSGGDVT-CCQTRVCFDQFALYKES--DFAFYKNPER- 159

Db 121 EPAGLRBPPLSVSPSPVAVAGENVTL-LLCCSNKRTDPLLSKEGAARPLRLSQDDG 180

QY 160 WPAAPPTLVTAAGSGYRCYFSSSDPYLWSASDFLELVYVTSITPSKLFTEPPSS 219

Db 181 WYQAFSS-SPVTAAGCYRCYRSLSTPPLLSGSEPLALVAD----- 225

QY 220 VAEFSPATLVLVSTNKKVFTETSRSTITSTKEGSDSAGPARQYTKGLVRCGAVI 279

Db 226 -----YTCNLIIRNGLASV 240

QY 240 LILAGFLAEQWHSRKRRLRHRGRAVGRPPLPLPOTRKSHG 324

Db 241 LLL-LGL-----LCCQRHDSG 257

A>Title: Genomic structures and chromosomal location of P91, a novel murine regulatory
 A/Reference number: J05894; M020:282-2938; PMID:9538215
 A/Accession: J05895
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-680 <YMG>
 A/Cross-references: GB:A04035; NID:92721691; PDB:1AB9627.1; PDB:92791692
 C/Comment: This protein function as inhibitory cell-surface molecule against cell activa
 C/Genetics:
 A/Map position: 7
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-119/Domain: extracellular Ig-like #status F
 F:120-119/Domain: transmembrane #status predicted <TM>
 F:120-680/Domain: cytoplasmic #status predicted <CT>
 Query Match 20.0%; Score 356.5; DB 2; Length 680;
 Best Local Similarity 22.9%; Pred. No. 15e-16;
 Matches 106; Conservative 50; Mismatches 111; Indels 135; Gaps 7;
 DB 22 SGRPKSLQJSSSLVPLEHVTLRCCGPPYDLPFLKSSRYQCAV-----73
 DB 220 SGNLQKRTIKAPSSVITGRKMTIKQGNLDAEYFLNEKQKSTGCTDQCPNKR 279
 DB 74 -FIPAKPSLAGRRCYONSLSLPSDCLVATVWA--KSLSLACGPVSSGCV 130
 DB 280 FFIISVTCQNGQRCYCYSAGSOSTLISLVTSYVNERLSLSPVRRPGNM 315
 DB 131 TCCQTRVGFDCPALYEGD-----PAPYKPERVYKASHPIITVPAHSQYRCYFS 164
 DB 340 TLHCASGCHYKFLITEDKKFANALDTEHSSPCQALFIISPTPTHTGRRCYGY 399
 DB 195 SRPVLWASPDPLDLYVTGTSTPS-----210
 DB 400 KMTQLWSVPSNLQQLISGLSKRPSLTHQGHLDPMGTLQCSGMYDGFALRWG 459
 DB 211 -----P 211
 DB 460 CADYCHSSQOTLGRVYANFTSGVSSSTGGQRCYGAHNLSSKASSEHLDLITCQ 519
 DB 212 LPTPESSV-----AF 222
 DB 520 LPTPSLSYQPHVHSGETVSLQMSMDVDTPLSKESAGQPLKSKSHQSQAE 579
 DB 223 FS-----EATRELVVSTFNKVFETRSITTSKES 254
 DB 580 FMSMAVTSLSGTRCYCAQDSFVLLSSASAPFELVTS-----GTESSSWPKRP 631
 DB 255 DSPAGPARQYTKNLVRCIGAVILLIAGFLNEDMSRRX 296
 DB 632 NPPIFENQCHTENTLIMGAVVVFVLSLILAEWRSHQ 673
 RESULT 9
 G31925
 KIR (CL-1) NK receptor precursor protein - human
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1995 #sequence revision 36-Jun-1997 #text change 05-Nov-1999
 C/Accession: J01925; 161726
 R/Magnum, N.
 submitted to the EMBL Data Library, June 1995
 A/Reference number: G08752
 A/Accession: G01925
 A/Status: preliminary; translated from GB/EMBL/DDJ
 A/Molecule type: mRNA
 A/Residues: 1-444 <WAG>
 A/Cross-references: EXBL:J03274; NID:910436C; PDB:1AB32522.1; PDB:910436I
 R/Colonna, M.; Samaridis, J.
 Science 266, 405-408, 1995
 A>Title: Cloning of immunoglobulin superfamily members associated with HLA-C and HLA-B
 A/Reference number: A56241; M020:95232526; PMID:7718543
 A/Accession: 161726
 A/Status: preliminary; translated from GB/EMBL/DDJ
 A/Molecule type: mRNA

A/Residues: 1-444 <RES>
 A/Cross-references: GB:L41265; NID:9780307; PDB:1AA69670.1; PDB:9780308
 C/Genetics:
 A/Status: NKAT-3
 A/Map position: 19
 Query Match 18.8%; Score 335; DB 2; Length 444;
 Best Local Similarity 30.4%; Pred. No. 5.6e-17;
 Matches 112; Conservative 34; Mismatches 127; Indels 96; Gaps 12;
 DB 1 XPSPTALFCLQGLGVRP-----ACSGP-----FKPSQALPSSVFLKPYT 45
 DB 62 XSVPTALAGNTCGSPHPTGMSAKRPMVIMVTKNKPSSLAHGFLVKKGERVY 141
 DB 45 LRCQSPGVVDYLRLEKLSRRYQCAV-----JF-PAMKSLAGRYC-----88
 DB 142 LCKMDIMEHFFLHKRGLSDPSLVQCICHDGVSKAFPSGPMMLAAGTRCYGVTH 201
 DB 59 -SYNGSLKSLPSDCLVATGVFAKPSLSPGPAVSSGDDYTCQCTRYGQFALYK 147
 DB 202 TPYQ-----LSASDPLDIVTQPEKPSLSQPGKVDAGSVTSSSRSSVDMYH:SR 257
 DB 148 ECDPAPYKRP-----ERWPAFPITITVPAHSGTRCYFSRSSDPYVMSAFSDPLDLYV 202
 DB 256 ECGAHERLPVAVKXNRIFQADFLP--GPATHCGRYRCGSRHSRPYVMSDPLDLYSV 315
 DB 203 TQTSVTPSSLPPEPSSVAESEAFAELTVSTNKFVPTTE:RSALITTPKESDSPAQPAR 262
 DB 316 TG-----NPSSS-----WSPSTFSSSKSCKRPR 337
 DB 263 QYTKGNLVRIQLGAVILLIAGFLNEDMSRRXLRHGRVCPFLPPLPQTRKSH 322
 DB 338 HLMH---LIGTSVILIPFLFELSLMCKSKK-----NAVV-----MOGEFAGNRTA 383
 DB 323 GSDGGRCP 331
 DB 384 NSEDSDCD 392
 RESULT 10
 B33434
 Cell surface glycoprotein gp49s form 2 precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 19-May-1995 #sequence revision 19-May-1995 #text change 05-Nov-1999
 C/Accession: B33434
 R/Castells, M.C.; Wu, X.; Arm, J.P.; Austen, K.F.; Katz, H.R.
 J. Biol. Chem. 269, 8393-8401, 1994
 A>Title: Cloning of the gp49b gene of the immunoglobulin superfamily and demonstrati
 A/Reference number: A53434; M020:94179223; PMID:8132564
 A/Accession: B33434
 A/Status: preliminary
 A/Molecule type: DNA; mRNA
 A/Residues: 1-296 <CAS>
 A/Cross-references: GB:U05265; NID:9475446; PDB:1AA17795.1; PDB:9475448; GB:U05266;
 C/Genetics:
 A/Status: gp49b
 A/Accession: 12/3; 24/2; 119/2; 220/1; 232/1; 249/3; 272/1
 C/Keywords: alternative splicing; g-y-coprotein
 Query Match 18.5%; Score 330; DB 2; Length 296;
 Best Local Similarity 36.1%; Pred. No. 7.9e-17;
 Matches 86; Conservative 33; Mismatches 101; Indels 22; Gaps 6;
 DB 6 TALLFCGLCLGRVPAQSGPLPKPSLQALPSSLVLEKPYTLRCQSPFGVDLYRLEKLS 64
 DB 6 TVLLYLGLLISPRVAVQAGHLPKPIWLEFGSVLAATSVITWCGSWEAGCYHRYKES 65
 DB 65 SRYCD-----GAV-FIPAKRSLGRVCSYONSLSLPSDCLVATGVFAKPS 115
 DB 66 VNFMTQVLETRNKAQKPIPSYATTSYATVYCYESAAQSHSDAELVMTGAYENPS 125
 DB 116 LSAQGPVAVSSGDDYTCQCTRYGFDOPALYKSG-----DFAPYKPERVYKASHPI 167

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Db 126 USVYPSBNVTSGVSISSGSSSVFGRFLLIQEKHCLSLTLDSCQHPNGPSV--A-VVL 163
      |||
Cy 168 :TTTAASGTYRCISFSSRDPYLSAPSDPLEVYVGTSTPRLPTEPSSVAEF-SEA 226
      |||
Db 184 DAVTFNKTGTCRCYGRNERPQVSKSPNSLJLWISRTK-DQSGSTPREDASVKNQSEY 242
      |||
Cy 227 TAE 233
      |||
Db 243 NAE 246

RESULT 11
A:Accession: A56247
A:Species: Homo sapiens (man)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: A56247
R:Colonna, M.; Samaridis, J.
Science 268, 405-408, 1995
A:Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B
A:Reference number: A56247; MID:95232525; PMID:7716543
A:Accession: A56247
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-348 <RES>
A:Cross-references: GB:I41267; NID:G780303; PTDN:AAA62868.1; PID:G780304
C:Genetics:
A:Gene: GDB:NKAT1
A:Cross-references: GDB:698165
A:Map position: 19

Query Match
Best Local Similarity 30.1%; Score 328; DB 2; Length 348;
Best Local Similarity 30.1%; Pred. No. 1,2e-16;
Matches 101; Conservative 34; Mismatches 107; Indels 64; Gaps 12;

Cy 1 MSPSTALFCLGCT--GRVPAQSGPLPKPS-QALPSSVLPKPYTLCQGGPQVQVYR 58
      |||
Db 1 XSLIVSVACVGFLLCGAMP--HEGVHRKPSLLAHPPVYKSEETVILQCMWDVFEHFL 59
      |||
Cy 59 LEKUSSRYCD-----CAVLEFPAMKRSIAGRYC-----SYNGSLWS 98
      |||
Db 60 LHR--FGMFDTLTGLGHHGCVSKANFSISMTQDIAGTYRCVGSVTHSFYQ---VSA 113
      |||
Cy 99 PSQGLELVATGVFAKPSLSAQPGVAVSSGGVLT-QCCTRYGFQDPALYKGDPAKYPK 157
      |||
Db 114 PSDPLJLVITGLYKPSLSAQPGVAVSSGGVLT-QCCTRYGFQDPALYKGDPAKYPK 173
      |||
Cy 158 -----ERVYRASFPITITVAAGSTYRCVSPSSRDPYLSAPSDPLEVYVGTSTPRLP 213
      |||
Db 174 GPKNGTGFQADPFL--GATHTGTYRCGSHSPYKSKSSDFLLVSYGNPSKNSP 231
      |||
Cy 214 TEPSSVAEFSEATAEITVSTKNVFTTETRSITTFKESDPSFAGPAPCYTKGTVRI 273
      |||
Db 232 TEPSSK-----TGNFPR-----LHI 246
      |||
Cy 274 CLG---AVILITLQGLAEKMSRK 296
      |||
Db 247 LIGTSVAILFLIFLFLDHKCSNKK 272

RESULT 12
A:Accession: G01924
A:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: G01924; G01945
R:Wagman, K.
Submitted to the EMBL Data Library, June 1995
A:Reference number: G01924
A:Accession: G01924
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

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A:Residues: 1-444 <WAG>
A:Cross-references: EMBL:U32973; NID:G1004359; PTDN:AA82522.1; PID:G1004359
R:D Andrea, A.; Chang, C.; Franz-Bacon, K.; McCannan, T.; Phillips, C.H.; Janier,
submitted to the EMBL Data Library, July 1995
A:Reference number: G08908
A:Accession: G01945
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-444 <DXA>
A:Cross-references: EMBL:U31416; NID:G973405; PTDN:AAQ3725.1; PID:G973406
C:Genetics:
A:Gene: NKX1

Query Match
Best Local Similarity 30.1%; Score 327; DB 2; Length 444;
Best Local Similarity 30.1%; Pred. No. 2,1e-16;
Matches 112; Conservative 34; Mismatches 128; Indels 96; Gaps 12;

Cy 1 MSPSTALFCLGCTGVRP-----AQSGP-----PKFSIQA-PSSVLPKPYT 45
      |||
Db 52 MSPV-TTAAGNVTGCSHPSPTGSAQSNPVVIVTGNHKKPSLLAHGCPVNSGERVI 141
      |||
Cy 46 LRCGPPGVLYLEKUSSRYCQAV-----LTPAKYKSLAGRYC-----88
      |||
Db 142 LCCWMDIMFEHFLLKREGISKDPSRLVQCIHDVSKANFS-CQPMMLAAGTYRCVSVTH 201
      |||
Cy 89 -SYNGSLWS-PSQGLELVATGVFAKPSLSAQPGVAVSSGGVLT-QCCTRYGFQDPALYK 147
      |||
Db 202 TPIQ---LSAFSDPLD-VVITSPYKPSLSAQPGVAVSSGGVLT-QCCTRYGFQDPALYK 257
      |||
Cy 148 ESDPAPYKNP-----ERVYRASFPITITVAAGSTYRCVSPSSRDPYLSAPSDPLEVY 202
      |||
Db 258 EKGAFERRLPAYKRYR-FQADPFL--GATHTGTYRCGSHSPYKSKSSDFLLVSYGNPSKNSP 315
      |||
Cy 233 TSTVTPSKRLPTEPSSVAEFSEATAEITVSTKNVFTTETRSITTFKESDPSFAGPAPK 262
      |||
Db 316 TG-----KPSSS-----WPEPTFSSKSGNPR 337
      |||
Cy 263 CYTGNVLR-CLGAVIITLGLFAEDPSRKRLLRHGRAVQSPLEPPLPGRKSH 322
      |||
Db 338 HLHI---LIGTSVAILFLIFLFLDHKCSNKK-----NAV-----NDGEPAGNRHA 383
      |||
Cy 323 GQDGGRCQ 331
      |||
Db 354 NSDDSDCCQ 392

RESULT 13
A:Accession: U32973
A:Species: Homo sapiens (man)
C:Date: 23-May-1996 #sequence_revision 23-May-1996 #text_change 05-Nov-1999
C:Accession: U32973
R:Colonna, M.; Samaridis, J.
Science 268, 405-408, 1995
A:Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B
A:Reference number: A56247; MID:95232526; PMID:7716543
A:Accession: A56247
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-341 <RES>
A:Cross-references: GB:I41268; NID:G780305; PTDN:AAA69869.1; PID:G780306
C:Genetics:
A:Gene: NKAT-2

Query Match
Best Local Similarity 30.1%; Score 323.5; DB 2; Length 341;
Best Local Similarity 30.1%; Pred. No. 2,8e-16;
Matches 99; Conservative 36; Mismatches 105; Indels 89; Gaps 12;

Cy 1 MSPSTALFCLGCT--GRVPAQSGPLPKPS-QALPSSVLPKPYTLCQGGPQVQVYR 56
      |||
Db 1 XSLIVSVACVGFLLCGAMP--HEGVHRKPSLLAHPPVYKSEETVILQCMWDVFEHFL 59
      |||
Cy 59 LEKUSSRYCD-----CAVLEFPAMKRSIAGRYC-----SYNGSLWS 98
      |||

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Db      60 LHR--EGKFKDTLHLIGEHHDGVGKANFS:GPMKQDLAGYFRYGVSYTHSPYQ-----ISA 113
Qy      99 PSQDLVATGVFAKPS:SAQPSGAVSSGGVLTQCTRYGDFQFALYKED-----P 151
Db      114 PSDPLDVLITGLYKRPDLSAQPGPTVLAGESTLSCSSRSYDMYHLSRGEAHKRRFSN 173
Qy      152 APYKPRRWYRASPIITVTAASGYTCYSSSRDPYJMSAPCELELVYTGTSYTFST 211
Db      174 GPKNVGT--FOADEPFL--GPATHGCTYRCFGSPFSDSYEMWSNSDPLVSVTGKPSNWP 229
Qy      212 LPTPEPSSVAEFSNATDELTVSFTNKVFTTETESSTTSFKESDSPAGPARYTKGNLY 271
Db      230 SPTEPSSSE-----TGKPRH-----L 244
Qy      272 RICLGA---VITILAGF--AEQWHSRRX 296
Db      245 HVLGTGTVLITFLLEPFLHRCCKNK 273

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RESULT 14

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709402
C:Accession: T09402
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision: 11-Jun-1999 #text_change: 21-Jul-2000
C:Accession: T09402
C:Mazzarella, R.; Pengue, G.; Jones, C.; Schlessinger, D.
Genomic 48, 157-162, 1998
A:Title: Cloning and expression of an immunoglobulin superfamily gene (IGSF1) in XG25.
A:Reference number: 216655; NID:98195514; PMID:9521868
A:Accession: T09402
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1327 <MAZ>
A:Cross-references: EMBL:AF034198; NID:G2645889; PIDN:AAC520571; PID:G2645896
C:Genetics:
A:Gene: Igsf1
A:Map position: Xq25

```

```

Query Match      18.0%; Score 322; DB 2; Length 1327;
Best Local Similarity 32.1%; Pred. No. 1,86-15;
Matches 105; Conservative 37; Mismatches 133; Indels 52; Gaps 9;

```

```

Qy      26 PKRSJALPESVLEKPVLTICQPP--PVDLYLLEKSSSY----QDQAVYFPAY 75
Db      960 PKPWCFAPPSVEMGQVTLMOCPVHGVYLHKEGEATSCQDMGSTNDGAFPTN 1019
Qy      79 KSLAGRRRCQSYO--NSGLMSLPDQLELVATGVPAKPS:SAQPSGAVSSGGVLTQCT 135
Db      1020 SGTSMGRISCCYHEDMSSKIQPSNTLELVTLGDPKPS:LAQPGPVAVAGENMTQCO 1079
Qy      136 TRYGDFQFALYKED--DPAYKNPERWYRASFPITVTAASGYTCYSSSRDPYJMSA 193
Db      1080 GELPDSTFVLKESGCEPFCQGRPS--GYRAQFWKPAVAGEDSGYSCVYLDSTPFAASN 1138
Qy      194 PSDPLELVYTGTSVTPS-----RLPTPEPSSVAEF-----SEATDEL 221
Db      1139 HSDSLEIHWCKPKPSLSAWESTMFKLGKDIITQCGPLGVGVFVLEHDESAPOQFSE 1198
Qy      232 -----VSFTKXVFTTESPISITTSKESDSPAGPARYTKGNLYTCL 275
Db      1139 DGEFVINNVEGKIGNCSYPLCAVPSDKSPSDPLEJVGAAQPVVAQECTVSNIVSSSL 1256
Qy      276 GAVILITLIGFLADWHSRRKRLRRRG 302
Db      1259 IVVVVVAGVVLAEK--KKMPRLRTRG 1264

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RESULT 15

```

A53434
Cell surface glycoprotein gp49b form 1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1995 #sequence_revision: 19-May-1995 #text_change: 05-Nov-1999

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C:Accession: A53434
R:Castells, M.C.; Wu, X.; Aron, J.F.; Austen, K.F.; Katz, H.R.
J. Biol. Chem. 269, 8393-8401, 1994
A:Title: Cloning of the gp49b gene of the immunoglobulin superfamily and demonstration
A:Reference number: A53434; NID:94179223; PMID:8132564
A:Accession: A53434
A:Status: preliminary
A:Molecule type: DNA; mRNA
A:Residues: 1-335 <CAS>
A:Cross-references: GB:U05265; NID:9475446; PIDN:AAA17797.1; PID:9475447; GB:U05264;
A:Gene: gp49B
A:Accession: 12/3; 24/2; 119/2; 220/1; 232/1; 271/1; 268/3; 311/1
C:Keywords: alternative splicing; glycoprotein

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Query Match      17.9%; Score 317.5; DB 2; Length 335;
Best Local Similarity 34.0%; Pred. No. 7,5e-16;
Matches 84; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

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Qy      6 TATFCLSLCLGRVPAQSGFLPKPSLQALSSSLVPLEKPVLTICQPGPQVLYRLEKSS 64
Db      6 TVALYLGLLEPRITVAQGHLPKPIVAEPGSVIAAYTSVITKCGSWEACVYHLYKXS 65
Qy      65 SRYOD-----CAVLFIPMKRSLAGRYPCSYONGSLMSLSDQLELVATGVFAKPS 115
Db      66 VNPMTQVPLETRNKAKEKTSMTSYAGIKCYTESAAGESEHSDAMELVYTGAYENPS 125
Qy      116 LSNQGPVAVSSGGVTLQCTRYGDFQFALYKED-----DPAYKNPERWYRASFP 167
Db      126 LSVYSSSVNTGSVSTSSSCSSSYVGRFILLQEGKHSWMLDSQHCAHQNSY--ATFLV 183
Qy      165 TTVTAASGYTCYSSSRDPYJMSAPCELELVYTGTSVTPERAFTEPPESSVAEFSNAT 227
Db      184 DAVTPNHNQTPRCYCFPNEPQVMSKPSNLDLMSETK--DQSSPTPE--DGLTYQKIL 240
Qy      228 AETVTSF 234
Db      241 IGVLVSF 247

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Search completed: October 23, 2003, 09:43:01
Job time : 45 secs

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GenCore version 5.1.6
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CM protein - protein search, using SW model

Run on: October 23, 2003, 09:38:24 ; Search time 23 Seconds
(without alignments)
693.133 Million cell updates/sec

Title: US-09-503-387-3

Perfect score: 1786

Sequence: 1 XSPSPFALPCLGLGCRVPA.....KSHGQCGSRQDVHSGJCS 339

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Maximum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

Database: SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	392	21.5	287	1	FCAR_HUMAN
2	342.5	19.2	367	1	K3S1_HUMAN
3	340	19.0	377	1	K214_HUMAN
4	335	18.8	444	1	K312_HUMAN
5	330.5	18.5	304	1	K252_HUMAN
6	329	18.4	348	1	K212_HUMAN
7	325.5	18.2	304	1	K251_HUMAN
8	323.5	18.1	341	1	K213_HUMAN
9	320.5	17.9	304	1	K254_HUMAN
10	319	17.9	455	1	K312_HUMAN
11	317.5	17.8	335	1	K498_MOUSE
12	307	17.2	304	1	K255_HUMAN
13	299	16.7	334	1	K253_HUMAN
14	289.5	16.2	333	1	K499_MOUSE
15	289.5	16.2	333	1	K499_MOUSE
16	143.5	9.2	485	1	ALB1_HUMAN
17	136	7.6	231	1	DM43_DROME
18	126.5	7.2	3737	1	FCB1_MOUSE
19	123.5	6.9	267	1	FCG3_RAT
20	118	6.6	4391	1	FCB1_HUMAN
21	116	6.5	2774	1	MAP2_RAT
22	115.5	6.5	1739	1	SN_HUMAN
23	113.5	6.4	1284	1	NRGA_CHICK
24	108	6.3	257	1	FCB1_HUMAN
25	107	6.3	341	1	FCG3_CAVO
26	106.5	6.3	261	1	FCG3_MOUSE
27	106.5	6.3	3375	1	UN52_CAEEL
28	106	5.9	285	1	FCG3_RAT
29	106	5.9	739	1	VCA1_MOUSE
30	106	5.9	2161	1	SHK1_HUMAN
31	105.5	5.9	330	1	FCG2_MOUSE
32	104	5.8	447	1	AMBN_HUMAN
33	104	5.8	740	1	PEC1_PIG

34	104	5.8	1367	1	AMYE_YEAST
35	103.5	5.8	770	1	DAB2_HUMAN
36	102.5	5.7	912	1	ICAS_RABIT
37	101.5	5.7	727	1	PEC1_MOUSE
38	101	5.7	296	1	FCG2_BOVIN
39	101	5.7	404	1	FCG1_MOUSE
40	101	5.7	3149	1	TRG1_EBV
41	100.5	5.6	1051	1	PRK7_CHICK
42	100	5.6	739	1	VCA1_RAT
43	99.5	5.6	1887	1	RPR1_DROME
44	99	5.5	404	1	RACE_HUMAN
45	99	5.5	739	1	VCA1_HUMAN

ALIGNMENTS

RESULT:

FCAR_HUMAN STANDARD; PRT; 287 AA.
AC P24071; Q13603; Q15727; Q15728; Q92590;
DT 01-04-1992 (Rel. 2); Created;
DT 01-04-1992 (Rel. 2); Last sequence update;
DT 15-SEP-2003 (Rel. 42); Last annotation update;
DE Immunoglobulin alpha Fc receptor precursor (IgA Fc receptor) (CD89 antigen).
GN FCAR OR CD89.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RX MEDLINE=9107969; PubMed=2258659;
RA Maliszewski C.R., March C.J., Schoenborn M.A., Gimpel S., Shen J.;
RT "Expression cloning of a human Fc receptor for IgA."
RL "Exp. Med. 172:1665-1672(1990)."
RP 12;
RS SEQUENCE FROM N.A. (ISOFORM A.1).
RC TISUE=bone marrow;
PX MEDLINE=95163085; PubMed=7636189;
RA de Wit T.P.M., Morton H.C., Capel P.C.A., van de Winkel G.G.J.;
RT "Structure of the gene for the human myeloid IgA Fc receptor (CD89)."
RL "Immunol. 155:1203-1209(1995)."
RN 13;
RX SEQUENCE FROM K.A. (ISOFORMS A.2 AND A.3).
RC TISUE=Alveolar macrophage, and Yorcocytes;
PX MEDLINE=56247667; PubMed=866819;
RA Parry C., Stille Y., Lehen A., Montreio R.C.;
RT "Identification of Fc alpha receptor (CD89) isoforms generated by alternative splicing that are differentially expressed between blood monocytes and alveolar macrophages."
RL "J. Immunol. 156:4442-4448(1996)."
RN 14;
RX SEQUENCE FROM N.A. (ISOFORMS B AND B-DELTA-52).
RA van Dijk T.B., Morton H.C., Caldenhoven E., Ruyck M., Raaijmakers J.A.M., Lamers J.W.C., Koederman J., Groot R.P.;
RL "Submitted (May-1996) to the EMBL/GenBank/DBJ databases."
RN 15;
RX SEQUENCE FROM N.A. (ISOFORM A.3).
RA MEDLINE=96433090; PubMed=8836118;
RA Pleass R.J., Andrews P.D., Kerr M.A., Woolf C.M.;
RT "Alternative splicing of the human IgA Fc receptor CD89 in neutrophils and eosinophils."
RL "Biochem. J. 318:771-777(1996)."
RN 16;
RX SEQUENCE FROM N.A. (ISOFORM J02).
RA Toyabe S., Kuwano Y., Takeeda K., Uchiyama M., Abo T.;
RT "Alternatively spliced forms of monocyte IgA Fc receptors in patients with IgA nephropathy."
RN 17;
RX Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN 17;
RX SUBUNITS.

```

RX METLINE=84375897; PubMed=7522255.
RA Pfleiderer L.C., Yeaman G.R.
R "Association of IgA-Fc receptors (Fc alpha R) with Fc epsilon RI
RT gamma 2 subunits in U937 cells. Aggregation induces the tyrosine
R phosphorylation of gamma 2."
R J. Immunol. 153:3228-3236(1994).
CC -1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN ALPHA.
CC MEDIATES SEVERAL FUNCTIONS INCLUDING CYTOKINE PRODUCTION.
CC INDUCING TYROSINE PHOSPHORYLATION OF GAMMA 2.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (FORM A) AND SOLUBLE
CC (FORM B).
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms=6;
CC Constitutive: Alternative isoforms seem to exist;
CC Name=A.1
CC IsoId=P24071-1; Sequence=Displayed;
CC Name=A.2
CC IsoId=P24071-2; Sequence=VSP_0024935;
CC Name=A.3; Synonyms=RIA2;
CC IsoId=P24071-3; Sequence=VSP_002634;
CC Name=B;
CC IsoId=P24071-4; Sequence=VSP_002636;
CC Name=delta-S2;
CC IsoId=P24071-5; Sequence=VSP_002632, VSP_002636;
CC Name=U02;
CC IsoId=P24071-6; Sequence=VSP_002633, VSP_002635.
CC -1- TISSUE SPECIFICITY: DIFFERENTIALLY EXPRESSED BETWEEN BLOOD AND
CC MONOCYTE, MYELOID CELLS. MONOCYTES EXPRESS ISOFORMS A.1, A.2 AND A.3
CC WHILE ALVEOLAR MACROPHAGES EXPRESS A.1 AND A.2 TRANSSCRIPTS;
CC HOWEVER THEY EXPRESS ONLY ONE ISOFORM AT THEIR SURFACES.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 2 Immunoglobulin-like C2-type domains.
CC -1- DATABASE: NMR=PROV, NMR=CD guide CDB entry.
CC WWW=HTTP://WWW.NCBI.NLM.NIH.GOV/PROV/CD/CDB3.HTM".
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CC or send an email to license@isb-sib.ch).
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DR EXBL: X34150; CAA38089.1; -.
DR EMBL: X87767; CAA61039.1; JOINED.
DR EMBL: X87768; CAA61039.1; JOINED.
DR EMBL: X87769; CAA61039.1; JOINED.
DR EMBL: X87766; CAA61039.1; JOINED.
DR EMBL: X67765; CAA61039.1; JOINED.
DR EMBL: U43774; AAC50639.1; -.
DR EMBL: U43677; AAC50595.1; -.
DR EXBL: U56236; AAB00566.1; -.
DR EXBL: U56237; AAB00567.1; -.
DR EXBL: S82919; AAD14421.1; -.
DR EMBL: D87859; BA13477.1; -.
DR F1F: G02630; G02630.
DR PIR: JHC332; JHC332.
DR HSSP: P43626; INKR.
DR Genew: H5KX1609; FCAR.
DR MIM: 147345; -.
DR GO: G0305887; C:intracel. to plasma membrane; TAS.
DR GO: G0305955; P:immune response; TAS.
DR InterPro: IPR003593; IG_MHC.
DR InterPro: IPR003596; IG_MHC.
DR Pfam: PF00347; Ig_2.
DR SMART: SMC0409; IG_2.
DR PROSITE: PS0835; IG_LIKE; FALSE NEG.
KW Receptor; Glycoprotein; Transmembrane; IgA-binding protein;
KW Immunoglobulin domain; Repeat; Signal; Alternative splicing.
FT SIGNAL 1 21 POTENTIAL
FT CHAIN 22 287
FT DOMAIN 22 227 IMMUNOGLOBULIN ALPHA FC RECEPTOR.
FT EXTRACELLULAR (POTENTIAL).

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FT	TRANSMEY	229	246	POTENTIAL.
FT	DOKAIN	247	287	CYCLOPLASMIC (POTENTIAL).
FT	DOKAIN	42	187	IG-LIKE C2-TYPE 1.
FT	DOKAIN	135	200	IG-LIKE C2-TYPE 2.
FT	DISULFID	49	130	BY SIMILARITY.
FT	DISULFID	146	193	BY SIMILARITY.
FT	CARBONYD	65	65	N-LINKED (GLCNAC . . .) (POTENTIAL)
FT	CARBONYD	79	79	N-LINKED (GLCNAC . . .) (POTENTIAL)
FT	CARBONYD	144	141	N-LINKED (GLCNAC . . .) (POTENTIAL)
FT	CARBONYD	177	177	N-LINKED (GLCNAC . . .) (POTENTIAL)
FT	CARBONYD	186	186	N-LINKED (GLCNAC . . .) (POTENTIAL)
FT	CARBONYD	198	198	N-LINKED (GLCNAC . . .) (POTENTIAL)
FT	VASPLIC	12	23	Missing (in isoform B-delta-52).
FT	VASPLIC	24	24	/Fld=VSP_002632.
FT	VASPLIC	24	24	G -> GRVSEHWCRSLGCGPNVDAAQAPRG (in isoform t02).
FT	VASPLIC	221	216	/Fld=VSP_002633.
FT	VASPLIC	195	216	Missing (in isoform A.3).
FT	VASPLIC	217	267	/Fld=VSP_002634.
FT	VASPLIC	217	267	Missing (in isoform A.2 and isoform J02).
FT	VASPLIC	217	267	/Fld=VSP_002635.
FT	VASPLIC	217	267	DSHSDVAFPSMCSMCOPGCLTFAETPVCK -> GRRRPVQ
FT	VASPLIC	217	267	ECPWVGCFPGGRAGI (in isoform B and isoform B-delta-52).
FT	VASPLIC	217	267	/Fld=VSP_002636.
SQ	SEQUENCE	287 AA;	32265 MW;	A2CCGA8467CD45F7 CRCE4;
Query Match		21.9%;	Score 392;	DB 1; Length 287;
Best Local Similarity		31.2%;	Pred. No. 4.7e-22;	
Matches 100;	Conservative	43;	Mismatches 110;	Indels 63; Gaps 50;
CY	MSPPPTLPFCIGLIG-RVPAQSCGLEPKPSLOCAPSSIVDPLEKPYTLRCOGPPGVGYR;	59		
CB	1 MDRPCQTLLCTVLIVDLGGRIQAQSGDDPMFP-SAKSSHPVLDGSVKIQCCAIREAVLTQC	60		
CY	ECFKLSSTRYOD-----CAYLFPRMKRLSIAGRYKRSYQNGSLNSLPSDDLFLVAT	108		
CB	61 KIKNKS-YFREGRRLKFENMETDPSPV-IDNDANKAGAYCCYRIGHYRFYSDDLFLVAT	120		
OY	:09 GVFAKPSLSADQGPVAVSOGCVTLQQCTRY-GPCDFALYKFGDPAPYKNFRWRASFPI	157		
CB	121 GYGRKPF-SARGYLVIKGENISILITCSAHIPPRFFSLAEGELSLPQHOSGHRPANFSL	190		
CY	168 ITVTAHSSTGYRCYSFSSRDPLYNASDCLELYVTSTSVTFSLPTFPSSVAEFGSAT	227		
CB	181 GPVLINWSGIYRCYGWNRSRYLWSPFNMLELVTT-----	216		
CY	228 AEIVVFSTNNKVTETLSRTSITSKESSDPAGPAROXYTKGNLRICGAVHLITLAGFI	267		
DB	217 -----DS-----HQDYTCNLIRMAVAGJLVALLAIL	245		
OY	268 AEDWHSRRKRLRHGRAYQR	308		
CB	246 VENNHSHTALKKEASADVAP	266		
RESULT 2				
K3SL_HUMAN				
ID_K3SL_HUMAN	STANDARD;	PRT;	387 AA.	
AC_Q14943;				
BT_01-NOV-1997 (Rel. 35, Created)				
BT_01-NOV-1997 (Rel. 35, Last sequence update)				
BT_15-SEP-2003 (Rel. 42, Last annotation update)				
TR_Killer cell immunoglobulin-like receptor 35s1 precursor (NCI class 1 NK cell receptor) [Natural killer associated transcritp 10] (NMAT-10);				
DE_KIR3DS1 OR NMAAT-10.				
OS_Homo sapiens (Human);				
OC_Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC_Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;				
OX_NCBI_TaxId=9606;				
RN_[]				
SEQUENCE FROM N.A.				

RX MEDLINE=96270034; PubMed=9662091;
 RX Boehring Co., Samaridis J., Co.oma M.,
 RT "Alternative spliced forms of human killer inhibitory receptors."
 RL Immunogenetics 44:227-230(1995).
 RN (2)
 RP VARIANT HIS-166;
 RX MEDLINE=98090286; PubMed=9410221;
 RX Thiberg M., Valiente N.M., Shum B.P., Shilling H.G.,
 RA Liebert-Waldenbach K., Cortiss P., Tian D., Janier L., Parham P.,
 RT "Human diversity in killer cell inhibitory receptor genes."
 RL Immunology 7:753-763(1997).
 CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
 CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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 CC EMBL: L76661; AAB36589.1;
 DR HSSP; P43526; INK.
 DR Genew; HGNC:6340; KIR3DS1.
 DR MIM; 604957;
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0003733; F:defense/immunity protein activity; NAS.
 DR GO; GO:0030106; F:MHC class I receptor activity; NAS.
 DR GO; GO:0036955; P:immune response; NAS.
 DR GO; GO:0030101; P:natural killer cell activation; NAS.
 DR InterPro; IPRO03539; 1g_MHC.
 DR Pfam; PF00347; 1g_3.
 DR SMART; SM00439; 1g_3.
 DR PROSITE; PS00835; IG-LIKE; FALSE NEG.
 KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KW Repeat; Multigene family; Polymorphism;
 KW SIGNAL; 1 21
 FT CHAIN 1 357
 FT DOMAIN 22 340
 FT TRANSMEM 341 363
 FT DOMAIN 364 387
 FT DOMAIN 388 410
 FT DOMAIN 411 433
 FT DOMAIN 434 456
 FT DISULFID 457 479
 FT DISULFID 480 502
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 FT CARBOHYD 572 594
 FT CARBOHYD 595 617
 FT CARBOHYD 618 640
 FT CARBOHYD 641 663
 FT CARBOHYD 664 686
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RT and HLA-B recognition by human natural killer cells." Science 268:405-408(1995).

RU (2)

RP SEQUENCE FROM N.A.

RQ TISSUE=Peripheral blood lymphocytes;

RA MEDLINE=9611967; PubMed=877725;

RA Magman N., Rajagopalan S., Kinter C.C., Peruzzi M., Jong E.C., "Killer cell inhibitory receptors specific for HLA-C and HLA-B identified by direct binding and by functional transfer." Immunity 3:801-809(1995).

RU (3)

RQ SEQUENCE FROM N.A.

RQ TISSUE=Peripheral blood lymphocytes;

RA MEDLINE=9643861; PubMed=8763894;

RA Pende D., Biassoni R., Cantoni C., Verdiani S., Falco M., di Donato C., Accame L., Bottino C., Moretta A., Moretta L., "The natural killer cell receptor specific for HLA-A allotypes: a novel member of the p58/p70 family of inhibitory receptors that is characterized by three immunoglobulin-like domains and is expressed as a 140-kD disulphide-linked dimer." J. Exp. Med. 184:505-518(1996).

RU (4)

RQ SEQUENCE FROM N.A.

RQ TISSUE=Blood;

RA MEDLINE=95378652; PubMed=7650366;

RA D'Andrea A., Chang C., Franz-Bacon K., McCrath T., Phillips C.H., Lanier L.L., "Molecular cloning of NKBL, a natural killer cell receptor for HLA-B allotypes." J. Immunol. 155:2306-2310(1995).

RU (5)

RQ SEQUENCE FROM N.A. AND VARIANTS.

RA MEDLINE=9809086; PubMed=9430221;

RA Utherg M., Valiente N.M., Shum B.F., Shilling H.S., "Human diversity in killer cell inhibitory receptor genes." Immunity 7:753-763(1997).

RU (6)

RQ FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-B ALLLELE INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.

CC -1- CELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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CC

DR EMBL: L41269; AAA69870.1

DR EMBL: J03273; AAB52521.1

DR EMBL: J03274; AAB52522.1

DR EMBL: X94262; CAA63938.1

DR EMBL: J14146; AAC33725.1

DR EMBL: AF022049; AAB95322.1

DR F01: G01925; G01925.

DR HSSP: P43624; INKA.

DR Gene: HNC6338; KIR3DL1.

DR MIM: 604946

DR GO: GO:0005887; C: integral to plasma membrane; NAS.

DR GO: GO:0003793; F: defense/immunity protein activity; NAS.

DR GO: GO:0030109; F: HLA-B specific inhibitory MHC class I recep. . . ; NAS.

DR GO: GO:000955; F: immune response; NAS.

DR GO: GO:0030102; P: negative regulation of natural killer cell . . . ; NAS.

DR InterPro: IPR003593; Ig.

DR InterPro: IPR003006; Ig_MHC.

DR Pfam: PF00047; Ig_3.

DR SMART: SM00409; Ig_3.

DR PROSITE: PS00835; IG_LIKE; FALSE_NEG.

KM Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;

KM Repeat; Multigene family; Polymorphism.

FT SGNL 1 21 BY SIMILARITY.

FT CHAIN 22 444 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR 3DL1.

FT DOMAIN 22 340 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 341 360 POTENTIAL.

FT DOMAIN 361 444 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 442 122 IG-LIKE C2-TYPE 1.

FT DOMAIN 137 282 IG-LIKE C2-TYPE 2.

FT DOMAIN 237 382 IG-LIKE C2-TYPE 3.

FT DISULFID 49 95 BY SIMILARITY.

FT DISULFID 144 295 BY SIMILARITY.

FT DISULFID 244 293 BY SIMILARITY.

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FT CARBOHYD 179 179 N-LINKED (GLUCNA. . .) (POTENTIAL).

FT CARBOHYD 273 273 N-LINKED (GLUCNA. . .) (POTENTIAL).

FT VARIANT 2 2 S -> L.

FT VARIANT 13 13 /FTID=VAR_010319.

FT VARIANT 23 23 /FTID=VAR_010320.

FT VARIANT 23 23 M -> V.

FT VARIANT 68 68 /FTID=VAR_010321.

FT VARIANT 68 68 S -> V.

FT VARIANT 75 75 /FTID=VAR_010322.

FT VARIANT 75 75 I -> L.

FT VARIANT 259 259 /FTID=VAR_010333.

FT VARIANT 259 259 G -> R.

FT VARIANT 333 333 /FTID=VAR_010336.

FT VARIANT 333 333 S -> C.

FT VARIANT 333 333 /FTID=VAR_010344.

FT VARIANT 333 333 /FTID=VAR_010345.

SC SEQUENCE 444 AA; 45398 MW; 47DEA12BBAFDEC53 CRC64;

Query Match 18.8%; Score 335; DB i; Length 444;

Best Local Similarity 30.4%; Pred. No. 1,36-17;

Matches 112; Conservative 34; Mismatches 127; Indels 96; Gaps 12;

CY 1 MSPPALFCLCLGVR-----AAGCL-----DPQLQAPSLVPEKVT 45

DB 92 MSVYTAAGNTGSHGSHPTGSAFSPVIVWYTHAKRPSLLHPGLVKGGRV 141

CY 46 LRCGSPGVDRLEKLSRRYQDAV-----LIPAKRSVAGRYQ----- 88

DB 142 LQWSDIWEHEFLKREGISKPSKWCQIHGVSKAPPSLGMMLALAGVRYGQSYTH 201

CY 89 -SYONSLSLSSDCELVATVFAKPSLSNCPGSAVSGCVTLCCQTRVGFDFALYK 147

DB 202 TPY-----LSASDFDQVYTGPRKPSLSAAGPKVAGSVTSCSSRSSVCMYRCSR 257

CY 148 EGVFAVYKRP-----EWYRASFPITTLAHSQTYCVSPSSRDYVMSAFDPLELVY 202

DB 258 EGVHERRRFAVRKXNRTQADPL--GPATHGCTYRCPGSRHSPYEMKSPSPDLVSV 315

CY 203 TGTSVTPSRLETPPSVAEPEENATLVTNKTFTTTSRSITTSKESDQFAGQAR 262

DB 316 TG-----NPSS-----WPSSTPSSKSKNFR 337

CY 263 CVYTKGVYRICGAVITLILAGFLAEWHSRKLRRGRVQVCPPLPQTRKSH 322

DB 338 HLH-----LGTSVITLILFLHLMCSKK-----NAV-----MDCPAGNRTA 383

CY 323 GGDGGRGQ 331

DB 384 NSRSDSDQD 392

RESULT 5

K2S2_HUMAN STANDARD; PRT; 304 AA.

AC P43631; Q14955;

CD 01-NOV-1995 (Rel. 32, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Killer cell immunoglobulin-like receptor 2D52 precursor (MHC class I

DE NK cell receptor) (Natural killer associated transcript 5) (NKAT-5)
 DE (p58 natural killer cell receptor clone C2-49) (p58 NK receptor) (NK
 DE receptor 183 Act1).
 GN KIR2DS2 OR NKAT5.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
 RX MEDLINE=95269128; PubMed=7749980;
 RA Wagtmann N., Blasson R., Cantoni C., Verdiani S., Valzani M.S.,
 RA Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
 RT "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
 RT related molecules with diversity in both the extra- and intracellular
 RT domains".
 RT Immunity 2:439-449(1995).
 RN 1;
 RP SEQUENCE OF 2-334 FROM N.A.
 RC TISSUE=Natural killer cell.s;
 PX MEDLINE=95269128; PubMed=7749980;
 RA Wagtmann N., Blasson R., Cantoni C., Verdiani S., Valzani M.S.,
 RA Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
 RT "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
 RT related molecules with diversity in both the extra- and intracellular
 RT domains".
 RT Immunity 2:439-449(1995).
 RN 1;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphoid;
 PX MEDLINE=96195217; PubMed=8627176;
 RA Blasson R., Cantoni C., Falco M., Verdiani S., Bottino C., Vitale M.,
 RA Corle R., Poggi A., Moretta A., Moretta L.;
 RT "The human leukocyte antigen (HLA)-C specific 'activatory' or
 RT 'inhibitory' natural killer cell receptors display highly homologous
 RT extracellular domains but differ in their transmembrane and
 RT intracytoplasmic portions".
 RT J. Exp. Med. 183:645-650(1996).
 RN 1;
 RP FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA C ALLELES.
 CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA C ALLELES.
 CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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 DR EMBL: U24979; AAC50338.1; A.T. INIT.
 DR EMBL: U41947; AA65425.1; .
 DR EMBL: X89653; CA61983.1; .
 DR HSSP: P43626; INK.
 DR Genew: HGNC:5334; KIR2DS2.
 DR MIM: 604953; .
 DR GO: GO:0016032; C: integral to membrane; NAS.
 DR GO: GO:0004888; F: transmembrane receptor activity; NAS.
 DR GO: GO:0006955; P: immune response; NAS.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR03006; IG_MHC.
 DR Pfam: PF00047; IG_2.
 DR SMART: SM00409; IG_1.
 DR PROSITE: PSS0835; IG_1; KE: P43626; F: transmembrane;
 KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 FT SIGNAL: 1.
 FT CHAIN: 22 304 BY SIMILARITY.
 FT KILNER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
 FT 2232.
 FT UPAIN: 22 245 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM: 246 263 POTENTIAL.
 FT DOMAIN: 266 304 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN: 42 107 IG-LIKE C2-TYPE 1.

FT DOMAIN: 142 205 IG-LIKE C2-TYPE 2.
 FT DISULFID 49 100 BY SIMILARITY.
 FT DISULFID 149 198 BY SIMILARITY.
 FT CARBOHYD 84 84 N-LINKED (GLCNAC) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC) (POTENTIAL).
 FT CONFLICT 20 20 W -> G (IN REF. 3).
 SQ SEQUENCE 304 AA; 186 CDDDDDEBA28 CRC64;
 Query Match 18.5%; Score 330.5; DB 1; Length 304;
 Best local similarity 33.1%; Pred. No. 1.7e-17;
 Matches 111; Conservative 35; Mismatches 105; Indels 6; Gaps 12;
 QY 1 XSPSTALFCGLCG-GEVACGSP-LEKPSQALPSSVLEKPYTRCCQPPGVLYR 59
 DB 1 XSLMVSMACVFFPLAQAMP-HEGVHKKPSLLAPGLVKEETVILQCMGSAFHEHL 59
 QY 59 EKSSSRVQD-----QAVLFIPKXSLNRYNC-----SICNSIMSL 56
 DB 60 LHR--EGKIDTLH--GSHHDCVSKANSIGKXQCLAGTYRCYGSVTHSPYQ----JSA 113
 QY 99 PSDOLELVAAGVAFNPSSACPGPAVSSGCGVTLCCQTRYGCDQALYKEGD-----F 151
 DB 114 PSDPDLIVTGLYKNSLACQPTVLAGESVTLSCSPSSYDWMHLSSEGZHHPRISA 173
 QY 152 APYKPEKRYRASPTITVTAAGSTYRCYSSSDPYLNAKPSPLELVYTSVTSR 211
 DB 174 GRKYNGT--FQADPEL--GPAFHGYRFGSFRCSPEKNSGDFLLVSVGNSSNKP 229
 QY 212 PTEPSSVAFESE-----ATAELTVSF-----NK-----VPTTSRSLTS 250
 DB 233 SPTSPSSKNGPRHHLVIGTSVKIPTTLLFLFHHKCSKKNKAAVMDQPAQNRIVN 289
 QY 251 PKESD 255
 DB 290 SEDSD 294
 RESULT 6
 ID K2L2 HUMAN STANDARD; PRT; 348 AA.
 AC P43627; Q14351;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Killer cell immunoglobulin-like receptor 2D2 precursor (MHC class I
 DE NK cell receptor) (Natural killer associated transcript 6) (NKAT 6)
 DE (p58 natural killer cell receptor clone C2-43) (p58 NK receptor).
 GN KIR2D2 OR NKAT6.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Natural killer cell.s;
 PX MEDLINE=95269128; PubMed=7749980;
 RA Wagtmann N., Blasson R., Cantoni C., Verdiani S., Mainati M.S.,
 RA Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
 RT "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
 RT related molecules with diversity in both the extra- and intracellular
 RT domains".
 RT Immunity 2:439-445(1995).
 RN 1;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Natural killer cell.s;
 PX MEDLINE=96270004; PubMed=8662292;
 RA Bottino C., Samaridis J., Colonna M.;
 RT "Alternatively spliced forms of human killer inhibitory receptors".
 CC Immunogenetics 44:227-230(1996).
 CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C
 CC ALLELES. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING
 CC CELL LYSIS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

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CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC
DR EMBL: U24376; AAC50334.1; -
DR EMBL: U24376; AAC50334.1; -
DR PDB: 1EFX; 14-NOV-99.
DR PDB: 2DL2; 29-DEC-99.
DR PDB: 2DL1; 05-MAY-00.
DR Genew: HGNC:61330; KIR2DL2.
DR MIM: 604937; -
DR InterPro: IPR003599; IG.
DR InterPro: IPR003599; IG.
DR Pfam: PF00347; 19; 2.
DR SMART: SMO0409; 19; 2.
DR PROSITE: PS50835; IG_LIKE; FALSE NEG.
KM Receptor, immunoglobulin domain; glycoprotein; Signal; Transmembrane;
KM Repeat, Multigene family; 3D-structure.
FT CHAIN 1 21 BY SIMILARITY.
FT CHAIN 2 348 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT CHAIN 2DL2.
FT DOMAIN 22 245 EXTRACELLULAR (POTENTIAL).
FT TRANSXEM 245 264 POTENTIAL.
FT DOMAIN 265 348 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 107 IG-LIKE C2-TYPE 1.
FT DOMAIN 142 205 IG-LIKE C2-TYPE 2.
FT DISULFID 49 100 BY SIMILARITY.
FT DISULFID 149 198 BY SIMILARITY.
FT CARBOHYD 84 84 N-LINKED (GLCNAc) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAc) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAc) (POTENTIAL).
FT CARBOHYD 289 290 SE -> RQ (IN REF. 2).
SQ SEQUENCE 348 AA; 38472 MW; 5854C546F5CF3F5F CRC64;

Query March 18.44; Score 329; DB 1; Length 348;
Best Local Similarity 31.14; Pred. No. 2.6e-17;
Matches 102; Conservative 34; Xismatches 104; Indels 88; Gaps 12;

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AC P43626; Q41470;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2DL1 precursor [MHC class I
DE NK cell receptor] (Natural killer associated transcript 1) (NKAT-1)
DE (p58 natural killer cell receptor associated transcript 1) (p58 NK
DE receptor) (p58.1 MHC class-I specific NK receptor).
DE KIR2DL1 OR NKAT1 OR CD158A.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_taxid=9606;
RN 1
RF SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=95232526; PubMed=7716543;
RA Colonna M, Samaridis J,
RA "Cloning of immunoglobulin-superfamily members associated with HLA-C
RA and HLA-B recognition by human natural killer cells.",
RM Science 268:405-408(1995).
RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-45.
RC TISSUE=Natural killer cells;
RX MEDLINE=95269128; PubMed=7749980;
RA Wagtmann N, Blässon R, Cantor C, Verdiani S, Malnati M.S.,
RA Vitale M, Bottino C, Moretta L, Moretta A, Long E.O.,
RA "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RA related molecules with diversity in both the extra- and intracellular
RA domains.",
RT Immunity 2:439-449(1995).
RL 3
RP SEQUENCE FROM N.A., AND VARIANTS.
RX MEDLINE=98090086; PubMed=9430221;
RA Chabery V, Valiante N.M., Shum B, P, Shilling H.G.,
RA Liebert-Weidenbach K, Collins B, Yan D, Lanier L.L., Parham P.,
RA "Human diversity in killer cell inhibitory receptor genes.",
RL Immunity 7:753-763(1997).
RN 4
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 27-221.
RX MEDLINE=9743335; PubMed=9288975;
RA Fan Q.R., Mosyak L, Winter C.C., Wagtmann N, Long E.O., Wiley D.C.;
RT "Structure of the inhibitory receptor for human natural killer cells
RT resembles haematopoietic receptors.",
RL Nature 389:95-100(1997).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC
DR EMBL: U24376; AAC50334.1; -
DR EMBL: U24376; AAC50334.1; -
DR EMBL: AF022045; AAC50334.1; -
DR PIR: A56247; A56247.
DR PIR: INKR; 11-NOV-98.
DR PDB: 1IY9; 30-MAY-01.
DR Genew: HGNC:61329; KIR2DL1.
DR MIM: 604936; -
DR GO: GO:0005887; C: integral to plasma membrane; TAS.
DR GO: GO:0004872; F: receptor activity; TAS.
DR GO: GO:0006955; P: immune response; TAS.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003006; IG_MHC.

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CR Pfam: PF00047.1; 2.
CR SMART: SM00409.1; 1.
CR PROSITE: PS00635.1; 1.
CR Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
CR Repeat; Multigene family; Polymorphism; 3D-structure.
CR SIGMA: 2.
CR CHAIN 22 348
CR KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
CR 2D...
CR EXTRACELLULAR (POTENTIAL).
CR POTENTIAL.
CR CYTOPLASMIC (POTENTIAL).
CR 1G-LIKE C2-TYPE 1.
CR 1G-LIKE C2-TYPE 2.
CR DISULFID 49 100
CR DISULFID 149 198
CR CARBOHYD 67 67
CR CARBOHYD 84 84
CR CARBOHYD 144 144
CR CARBOHYD 178 178
CR VARIANT 5 5
CR VARIANT 37 37
CR VARIANT 135 135
CR VARIANT 175 175
CR VARIANT 184 184
CR VARIANT 203 203
CR VARIANT 237 237
CR VARIANT 266 266
CR STRAND 30 34
CR STRAND 38 40
CR TURN 41 42
CR STRAND 45 51
CR STRAND 57 63
CR STRAND 65 73
CR STRAND 75 77
CR TURN 78 79
CR STRAND 82 87
CR HELIX 92 94
CR STRAND 96 104
CR TURN 105 106
CR STRAND 107 107
CR TURN 108 109
CR STRAND 118 123
CR STRAND 130 134
CR STRAND 138 139
CR TURN 141 142
CR STRAND 144 151
CR STRAND 157 162
CR TURN 163 164
CR STRAND 168 172
CR STRAND 174 177
CR TURN 179 179
CR STRAND 183 185
CR STRAND 194 202
CR TURN 203 204
CR STRAND 205 209
CR STRAND 216 222
CR SEQUENCE 348 AA; 38504 MW; 3DBF2D6DCE1D1E C6C64;
Query Match 18.4%; Score 328; EB 1; Length 348;
Best Local Similarity 31.0%; Freq. No. 3.2e-17;
Matches 10%; Conservative 34; Mismatch 107; Indels 24; Gaps 11;
CY 1 NSPSPALFCLGLCL--GVSPGSGPGLKPSLQALPSLILYLERVTLKQSGPSCVLYR 58
DB 1.NSLIVVSACVGFLLQGANP--HESVHRKPSLALPGLVASEETVLIQCSVDFEFPJ 55

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CY 59 LEKSSRYOD-----DAVLFPAKRSAGRYRC-----SYNGSLMS; 98
DB 60 LHR--EGMENDTLRLGHHHDGSKANFSLSRMTQDLAGYRCVSVTSPPY----VSA 113
CY 99 PSDQLVATGVAFKPSLSAQSPAVSSGSDVTLQCYTRGVPQFALYKEGDFAPKAP- 157
DB 114 PSDLDIVITIGLYEKPSLSAQPGFVLASGVNTLSCSSRSRYDYNHLSREGAHERLPA 173
CY 153 ---ERNYRASFPTITTAASGTYRCYSSSRDPYLMSAPDPELVYTGSTVTPSRAP 213
DB 174 GPKRNGTFQACFPL--GPAFHGTYRCGSPFHDSPYKSSSDPLVSVTGPNKSPSP 231
CY 214 TEPSSVAERSEATAEATVSPFNKVFTEERSIITSPKESDSPAAGACQYTKGNVRSI 273
DB 232 TEPSSK-----TANPRA-----LHI 246
CY 274 CG---AVILITLAFLEDMHSRK 296
DB 247 LIGTSVYLFLFLFFLLMRCSMK 272
RESULT 8
K2S1 HUMAN
ID K2S1 HUMAN STANDARD; PRT; 304 AA.
AC Q24954; Q43471;
DC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DR 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2DS1 precursor (MHC class I
DE NK cell receptor Ede Act1).
UN KIR2DS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI_TaxID=9606;
PY 11.
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=96195217; PubMed=6627176;
RA Slasson R., Cantoni C., Falco M., Verdiani S., Bottino C., Vitale M.,
RA Conte R., Poggi A., Moretta A., Moretta L.;
RT "The human leukocyte antigen (HLA)-C-specific 'activatory' or
RT 'inhibitory' natural killer cell receptors display highly homologous
RT extracellular domains but differ in their transmembrane and
RT intracytoplasmic portions."
RT J. Exp. Med. 183:645-650(1996).
EN [2]
SEQUENCE FROM N.A. AND VARIANT LYS-91.
RX MEDLINE=98090886; PubMed=9433221;
RA Thiberg M., Valiente N.M., Strom B.P., Stalling H.G.,
RA Liebert-Weddenbach K., Gsellus B., Ryan D., Lanier L.J., Parham P.;
RT "Human diversity in killer cell inhibitory receptor genes."
RL Immunity 7:753-763(1997).
CC 1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC 1- SUBCELLULAR LOCATION: Type I membrane protein.
CC 1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC 1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC
CY EMBL: X69892; CAA61982.1;
CY EMBL: AF022046; AAB933.9.1;
CY HSSP: P43626; INKR.
CY Genes: HSN6333; KIR2DS1.
CY XIM: 604952; -.

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RA	Colinra M., Samaridis C.;
RT	"Cloning of immunoglobulin superfamily members associated with HLA-C
RT	and HLA-B recognition by human natural killer cells.";
RL	Science 268:405-408(1995).
RN	72
RP	SEQUENCE FROM N.A.
RC	TISSUE=Natural killer cells;
RX	MEDLINE=95269128; PubMed=7749980;
RA	Waters M., Vallante N.M., Shum B.P., Shilling H.G.,
PA	Lienert-Widchenbach K., Corliss B., Tyar D., Lanier L.L., Parham P.;
RT	"Human diversity in killer cell inhibitory receptor genes.";
RL	Immunity 7:753-763(1997).
CC	- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC	- INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC	- SUBCELLULAR LOCATION: Type I membrane protein.
CC	- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC	- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC	or send an email to licenses@isb-sib.ch).
CC	-----
DR	EMBL; L41268; AAA69969.1; ..
DR	EMBL; U24074; AAC50333.1; ..
DR	EMBL; AF022048; AAB95321.1; ..
DR	PIR; 161725; 161725.
DR	HSSP; P43626; INKR.
DR	Genew; HGNC:6331; KIA2DL3.
DR	MIM; 604938; ..
DR	GO; GO:0016021; C:integral to membrane; TAS.
DR	GO; GO:004872; F:receptor activity; TAS.
DR	GO; GO:006965; P:immune response; TAS.
DR	IntrPrd; IPRO03599; 29.
DR	IntrPrd; IPRO03005; Q_MHC.
DR	Pfam; PF00047; 19; 2.
DR	SMART; SMO0409; 1G; 1.
DR	PROSITE; PS00835; 1G LIKE; FALSE NEG.
KW	Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW	Repeat; Multigene family; Polymorphism
FT	SIGNAL 1 21
FT	CHAIN 22 341
FT	CDL1
FT	EXTRACELLULAR (POTENTIAL)
FT	POTENTIAL 245 265
FT	CYTOPLASMIC (POTENTIAL)
FT	DONAIN 266 341
FT	DONAIN 42 137
FT	DONAIN -42 205
FT	DISULFID 49 133
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	CARBOND 84 198
FT	CARBOND 178 178
FT	CARBOND 211 211
FT	VARIANT 9 9
FT	VARIANT 9 9
FT	/FTId=VAR_010313.
FT	L -> R.
FT	/FTId=VAR_010314.
FT	O -> E.
FT	/FTId=VAR_010315.
FT	H -> R.

Db 215 EPPSSVAESES-----ACALITVSTNNVP 239
 233 EPPSSKGNPRHJHVICISVXKIPETITLUF 262

RESULT 11
 K3L2_HUMAN STANDARD; FRT; 455 AA.
 AC K3L2_HUMAN Q14338; Q14347; Q14948; Q26844; Q95557;
 DT 01-NOV-1995 (Ref. 32, Created)
 DT 01-NOV-1995 (Ref. 32, Last sequence update)
 DT 15-SEP-2003 (Ref. 42, Last annotation update)
 DE Killer cell immunoglobulin-like receptor 3DL2 precursor (MHC class I NK cell receptor) (Natural killer cell associated transcript 4) (NKAT-4) (p70 natural killer cell receptor clone CL-5).
 GN KIR3DL2 OR NKAT4
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID:9606;
 RN 11
 RP TISSUE: Natural killer cells;
 RX MEDLINE:95232526; PubMed:7716543;
 RA Colombia M., Samadpour J.;
 RT "Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B recognition by human natural killer cells";
 RL Science 268:405-408(1995).
 RN 12
 RP SEQUENCE FROM N.A.
 RC TISSUE: Peripheral blood lymphocytes;
 RX MEDLINE:9611967; PubMed:8777725;
 RA Wagman N., Rajagopalan S., Winter C.C., Peruzzi M., Jong E.C.;
 RT "Killer cell inhibitory receptors specific for HLA-C and HLA-B identified by direct binding and by functional transfer";
 RL Immunity 3:801-809(1995).
 RN 13
 RP SEQUENCE FROM N.A. AND VARIANT VAL-113.
 RC TISSUE: Lymphoid;
 RX MEDLINE:96433861; PubMed:8768804;
 RA Pende D., Biasson R., Cantoni C., Verdiani S., Falco M., di Donato C., Accame L., Bottino C., Moretta A., Moretta L.;
 RT "The natural killer cell receptor specific for HLA-A allotypes: a novel member of the p58/p70 family of inhibitory receptors that is characterized by three immunoglobulin-like domains and is expressed as a 140-kD disulphide-linked dimer";
 RL J. Exp. Med. 184:505-518(1996).
 RN 14
 RP SEQUENCE FROM N.A.
 RX MEDLINE:96272004; PubMed:8662091;
 RA Downing C., Sarantis C., Colonna M.;
 RT "Alternatively spliced forms of human killer inhibitory receptors";
 RL Immunogenetics 44:227-230(1996).
 RN 15
 RP VARIANTS A1A-43; VAL-113; ASP-158; HIS-166; PRO-228 AND THR-252.
 RX MEDLINE:98090096; PubMed:9432281;
 RA Usherberg V., Vallianat N.M., Shui B.P., Shilling H.G., Lieberich W., Weidenbach K., Collier B., Ryan D., Hentzer J., Pathan F.;
 RT "Human diversity in killer cell inhibitory receptor genes";
 RL Immunity 7:753-763(1997).
 CC 1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-A ALLELES. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
 CC 2- SUBCELLULAR LOCATION: TYPE I transmembrane protein.
 CC 3- SIMILARITY: BELONGS TO THE IMMNOGLOBULIN SUPERFAMILY.
 CC 4- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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DR EMBL: 541373; AAA6997.1; -
 DR EMBL: U30372; AA652520.1; -
 DR EMBL: X93595; CA663792.1; -
 DR EMBL: X94373; CA664180.1; -
 DR EMBL: L76665; AA636593.1; -
 DR EMBL: L76666; AA636594.1; -
 DR HSSP: P43266; INKR.
 DR Gene: HNCN:6339; X-R3D2L2.
 DR K3M: 604947; 1; 3;
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0001922; F: MHC-interacting protein; TAS.
 DR GO: GO:0006968; P: cellular defense response; TAS.
 DR InterPro: IPR003599; 1;
 DR InterPro: IPR003066; 1; MHC.
 DR Pfam: PF00347; 1; 3;
 DR SMART: SMC0405; 1; 2;
 DR PROSITE: PS00935; 1; C: LIKE; FALSE_NEG.
 KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KW Repeat; Multigene family; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 455
 FT FT
 FT DOMAIN 22 343
 FT TRANSMEM 341 360
 FT DOMAIN 361 455
 FT FT
 FT DOMAIN 42 102
 FT DOMAIN 137 202
 FT DOMAIN 237 300
 FT DISULFID 49 95
 FT DISULFID 144 195
 FT DISULFID 244 293
 FT CARBOHYD 179 179
 FT CARBOHYD 239 239
 FT CARBOHYD 273 273
 FT CARBOHYD 306 306
 FT VARIANT 40 40
 FT FT
 FT VARIANT 113 113
 FT FT
 FT VARIANT 158 158
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 FT VARIANT 166 166
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 FT VARIANT 228 228
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 FT VARIANT 252 252
 FT FT
 FT SEQUENCE 455 AA; 50230 MW; D34BA6B6B3C2945 CRC64;
 SQ

Query Watch 17.9%; Score 319; DE 1; Length 455;
 Eest local similarity 30.7%; Pred. No. 2e-16;
 Matches 105; Conservative 44; X-matches 127; Incols 66; Gaps 15;

QY 1 MSPPTALFCLGLCL-GRVPACSGCPJPKFSLQJPSGLVPLJEXFVTLKCGGFGVLYR 58
 Db 1 NSLTIVSMACVGFLLCGAWPLVMGGO-DKPLSLAPSPVYVPRGCHVALQCHYRGRFNEM 59
 QY 59 LKXSSSR-----VCDQVAL-FTAMKRSLSARRCVYQNSL-----WSLPSDQ 102
 Db 60 LKEDRSVHVFIFRGRIFQESFIMGVPTAH---AGVRC---RGRHSILTGSAASNP 112
 QY 109 LCVATGVFAKSLSNQSPVASSGCVTLQCCRYGSDPVALYKESGPAPYKRPBRWY- 161
 Db 113 LCVMTGHRKSLAHGGLIKSGETIYDQMSVMEHFLRREGIS---EPPSRVLS 169
 QY 162 -----VASPFIITVTAHSGTYRCYSFSSRDYFLWSA9DPLELVATGTSVTPSRLLPT 214
 Db 170 QHDSVRKANFEGILGMLVLAGIVRCYGVSPHSYOLASNSDPAIDIVITGLYKPS-LSA 226

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CY 215 EPPSSVAEFSSEATLFTVTKVFTTE-----SRSLTTSKX-----ESGSPAPAPCY 264
DB 225 QPQPTVQAGENVTLSSGSSWSDYVHLSREGAHERRLAPVKNRATCAQFLOPA--- 265
CY 265 VTKGNLVERCLGAV-----LILLAGFLAEKWS 293
DB 266 -HGGTYR-CFGSFRALPCWKNSSDPLVSTGNPSSWPS 325

RESULT 12
349B-MOUSE
ID 349B-MOUSE STANDARD: PRT: 335 AA.
AC 064281; 064312;
DE 01-NOV-1997 (Rel. 35, Created);
DT 01-NOV-1997 (Rel. 35, Last sequence update);
DS 15-SEP-2003 (Rel. 42, Last annotation update);
GN Mast cell surface glycoprotein GP49B precursor;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
NCBI_TaxID:10090;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORMS GP49B AND GP49B2);
RC STRAIN:G14; 426 BALB/C; Tissue:Bone marrow;
RA KEDLINE:94119223; PubMed:812664;
RA Castelle X.C., Wu X., Ann J.P., Austen K.F., Katz H.R.;
RT Cloning of the GP49B gene of the immunoglobulin superfamily and
RT demonstration that one of its two products is an early-expressed "ast
RT cell surface protein originally described as GP49."
C1 Biochem. J. 265:8393-8401 (1994);
CC -1- FUNCTION: MAY PLAY A ROLE IN CELL-CELL OR CELL-CYTOXIC
CC INTERACTIONS DURING THE DEVELOPMENT OF MAST CELLS FROM MULTIPOTENT
CC PROGENITORS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event:Alternative splicing; Named Isoforms=2;
CC Name=GP49B1;
CC ISOID=064281-1; Sequence=Displayed;
CC Name=GP49B2;
CC ISOID=064281-2; Sequence=VSP 002510, VSP 002511;
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J05266; AAA17799.1; -
DR EMBL: U05265; AAA17797.1; -
DR EMBL: J05265; AAA17798.1; -
DR EMBL: J05264; AAA17796.1; -
DR PIR: A53434; A53434;
DR PIR: B53434; B53434;
DR HSSP: P43626; INKR;
DR MGD: MGI:152701; GP49B;
DR InterPro: IPR007110; Ig-like;
DR InterPro: IPR003006; Ig_MHC;
DR Pfam: PF00047; Ig_2;
DR PROSITE: PS50815; IG_LIKE; 1;
KW Signal; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW Alternative splicing;
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 335 MAST CELL SURFACE GLYCOPROTEIN GP49B.
FT DOVAIN 24 238 EXTRACELLULAR (POTENTIAL);
FT TRANSMEM 239 263 POTENTIAL;
FT DOVAIN 261 335 CYTOPLASMIC (POTENTIAL);
FT DOVAIN 42 125 IG-LIKE C2-TYPE 1;
FT DOVAIN 124 212 IG-LIKE C2-TYPE 2;
FT DISULFID 49 96 POTENTIAL;

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FT DISTULFID 144 156 POTENTIAL.
FT CARBOHYD 133 133 N-LINKED (GLNAC...) (POTENTIAL);
FT CARBOHYD 191 191 N-LINKED (GLNAC...) (POTENTIAL);
FT VARSLIC 232 232 G->D (in isoform GP49B2);
FT VARSLIC 233 271 /FTID=VSP002510;
FT VARSLIC 233 271 /FTID=VSP002511;
FT SEQUENCE 335 AA; 37544 MW; 6005186524E7876 CRC64;

Query Match 17.8%; Score 317.5; DB 1; Length 335;
Best Local Similarity 34.0%; Pred. No. 18e-16;
Matches 64; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

CY 6 TALFCGLQC-GRVACSGEFLKPELQALPSEVLVLEXVYLRCQGPVGLYRUEKUS 64
DB 6 TVLDYGLILERTAVQACHLKPFLMAPGCVANYSVITWCGSMFAQVHYKENS 65
CY 65 SRVQD-----QAVLFPMKSLAGRCISQNGSLNLPSCYFLVATVYFAKS 115
DB 66 VAPMDTQVLEFRNKAKEPIPMNTSYAGIYCYESMAGFSEHDAVELYMTGAYENS 125
CY 116 LSAQPGPAVSSGADVTLQCTRYGFDQFACVREG -----DPAFYKPEKWPASFPY 167
DB 126 LSVYPSNVTSGVSSISFSSSSIVFGFETLDEGCHGLSMTLDSCHQNKQSY--ATVVL 183
CY 166 TVTAAHSGITPCYSPSSSDPYLNSAPDFLELVATGTSVTPSRLLTPSPSVARESEAT 227
DB 164 EATPETHNCTPCYGFYRFPWERSKSLDLMSETR-DOSSPTE--DGLTYCKL 240
CY 228 AEIVSF 234
DB 241 TGVVVF 247

RESULT 13
K255 HUMAN
ID K255 HUMAN STANDARD: PRT: 304 AA.
AC Q149E3;
DE 01-NOV-1997 (Rel. 35, Created);
DT 01-NOV-1997 (Rel. 35, Last sequence update);
DS 15-SEP-2003 (Rel. 42, Last annotation update);
GN Killer cell immunoglobulin-like receptor 2B5 precursor (MHC class II
GN NK cell receptor) (Natural killer associated transcript 3) (NKAT3).
CN KIR2DS5 OR NKAT3.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
NCBI_TaxID:9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE:96270004; PubMed:8662091;
RA Doherty C., Samadpour C., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors";
RL Immunogenetics 44:227-230 (1996).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U76672; AAB36500.1; -
DR HSSP: P43526; INKR;
DR Genbank: HGNC:6337; KIR2DS5;
DR KIM; 604956; -
DR GO: GO:0005887; C:integral to plasma membrane; NAS;

```

DR GO:0003011; F:HLA-C specific inhibitory MHC class I recep. : NAS.
 DR GO:0003035; F:Immune response; NAS.
 DR InterPro: IPR003593; IG.
 DR InterPro: IPR003066; IG_MHC.
 DR Pfam: PF00347; IG_2.
 DR SMART: SM0409; IG_2.
 DR PROSITE: PS50835; IG-LIKE; FALSE NEG.
 KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KW Repeat; Multigene family.
 FT SIGNAL 1 21
 FT CHAIN 22 304
 FT DOMAIN 22 245
 FT TRANSMEM 246 264
 FT DOMAIN 265 304
 FT DOMAIN 42 107
 FT DOMAIN 142 205
 FT DISULFID 49 100
 FT DISULFID 149 208
 FT CARBOHYD 67 128
 FT CARBOHYD 84 178
 FT CARBOHYD 178 223
 FT CARBOHYD 223 223
 S2 SEQUENCE 304 AA; 33644 MW; F0SD73BFA3DE35DB CRC64;
 Query Match 17.2%; Score 367; DB 1; Length 304;
 Best Local Similarity 29.6%; Pred. No. 9.4e-16;
 Matches 68; Conservative 34; Mismatches 97; Indels 78; Gaps 8;
 QY 27 KPSLQALPSLVLPLEKPYTLPCQCGPPQDLRLKELSSRRYQDCAV-----LFI 75
 DB 28 KESLHAPGSLVKSSEIVLQWSDVMEHFLHREGFNHTLIGEHIDYSKAFSI 87
 QY 76 PAKKSLAGRYRC-----SYNGSLWSLPSDQLELVATGFAKPSLSAQPGVSSG 128
 DB 28 GRMTQCLAGYRCVGSVTHSPYQ-----SAPSDPDLIVTLGYSKSLPAPGPTVLAGE 143
 QY 129 CVTLQCTFRYGFDOALYKKEFPAPYKPE-----ERNYKASFLPTITTAHSQTPCYST 183
 DB 144 SYTLSCSSRSSTDMHLSEGFHERRPAPKPKVRFQASPLDPAT--HGQAVRCPSS 201
 QY 144 SARCPYWSAPSDPELVATG-SVTPSLPTPEPSSVAEFSRAAEELVSFTKAVPTTET 243
 DB 202 FSDSPYEWKSKSDPLLVATGSSKMSKSPTEPSE----- 237
 QY 244 GSGITTSKRESDFGAPKRYTKNLYRICAVIL---ITLAGEVAEWSRRX 256
 DB 238 ---TGNPRH-----LHVIGTSVVKLPFTILPFLHKKCSNKK 273
 RESULT 14
 K2S3_HUMAN STANDARD; PRT; 304 AA.
 ID K2S3_HUMAN 014952; 030644;
 AC 01-NOV-1997 Rel. 35; Created;
 DT 01-NOV-1997 Rel. 35; Last sequence update;
 DT 15-SEP-2003 Rel. 42; Last annotation update;
 DE Killer cell immunoglobulin-like receptor 2D53 precursor [MHC class I
 DE NK cell receptor] (Natural killer associated transcript 7) (NKAT-7);
 GN KIR2DS3 CR NKA77.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NC NCBI_TaxID:9606;
 NX (1);_TaxID:9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98270004; PubMed=8662031;
 RA Coehring C., Samaridis J., Colonna M.,
 RT "Alternatively spliced forms of human killer inhibitory receptors";
 RJ Immunogenetics 44:227-230(1996).
 RN 12;
 RP SEQUENCE FROM N.A.
 RJ TISSUE=Lymphoid;

RA Biosort R.;
 RL Submitted (Apr 1996) to the EMBL/GenBank/DBJ databases.
 CC 1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA C ALLIELES.
 CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
 CC 1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC 1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC 1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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 DR EMBL: L76670; AAR36598.1;
 DR EMBL: X97231; CA65570.1;
 DR HSSP: P43626; INKR.
 DR Gensu; HGNC:6335; KIR2DS3.
 DR MIM: 604954;
 DR GO:0003887; C:integral to plasma membrane; TAS.
 DR GO:0003822; F:MHC-interacting protein; TAS.
 DR GO:0006968; P:cellular defense response; TAS.
 DR InterPro: IPR033006; IG_MHC.
 DR InterPro: IPR033006; IG_MHC.
 DR Pfam: PF03047; IG_2.
 DR SMART: SM0409; IG_2.
 DR PROSITE: PS50835; IG-LIKE; FALSE NEG.
 KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KW Repeat; Multigene family.
 FT SIGNAL 21 304
 FT CHAIN 22 304
 FT DOMAIN 22 245
 FT TRANSMEM 246 264
 FT DOMAIN 265 304
 FT DOMAIN 42 107
 FT DOMAIN 142 205
 FT DISULFID 49 100
 FT DISULFID 149 208
 FT CARBOHYD 67 128
 FT CARBOHYD 84 178
 FT CARBOHYD 178 223
 S2 SEQUENCE 304 AA; 33717 MW; 80693F79844F9E7E CRC64;
 Query Match 16.7%; Score 299; DB 1; Length 304;
 Best Local Similarity 35.2%; Pred. No. 3.7e-15;
 Matches 87; Conservative 27; Mismatches 93; Indels 40; Gaps 9;
 QY 1 MSPSPALFCCGL--CGRVPAQSGPLKPSIQALPSGLVLEKPYTCRCGPPGVVYR 52
 DB 1 KSLNIVSYACVGFVWLOGAMP-HGEFRKPSLHAPGLVLSSEVTLQCSQDWMFHFLL 59
 QY 59 EKLSSRYQD-----CAVLFIPAMKSLAGRYEC-----SYNGSLWSL 98
 DB 63 LHR--EGFHTDILGEGHIDYSKAFSIAMRDLGATYRCVGSVTHSPYQ-----PSA 113
 QY 93 PSDQLELVATGFAKPSLSAQPGVATGCGCRVGFCDALYKSD-----P 151
 DB 114 PSDPDLIVTGVEPSSLSAQPGPTVLGSEVTLSCSSVSYDMHJSTEDENHERRSA 173
 QY 152 APYKPKRYKRAFFIITVTAHSQTYACVSSSDPYLAPSDPELVATGTSVTPSR 211
 DB 174 GRKXNCT--FQADPFL--GPAVQSGTYRCFQSFHSPYEWKSKSDPLLVATGNSNWF 229
 QY 212 LPTSPS 218
 DB 230 STPEPS 236
 RESULT 15
 G43A_WOJSE

ID G49A_MOUSE STANDARD; PR: 303 AA.
 AC G61450;
 DT 01-NOV-1997 (Ref: 35, Created)
 DT 01-NOV-1997 (Ref: 35, Last sequence update)
 DT 15-SEP-2003 (Ref: 42, Last annotation update)
 DE Mast cell surface glycoprotein G49A precursor.
 OS G49A OR G49.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID:10330;
 RN [1]

RP SEQUENCE FROM N.A. AND SEQUENCE OF 24-45.

RC STRAIN=BALE/C; TISSUE=bone marrow;
 RX MEDLINE=91340742; PubMed=1714901;

RA Arm J.P., Gurish Y.F., Reynolds D.S., Scott H.C., Gartner C.S.,
 RA Austen K.F., Katz H.R.;

RT "Molecular cloning of gp49, a cell-surface antigen that is
 RT preferentially expressed by mouse mast cell progenitors and is a new
 RT member of the immunoglobulin superfamily.";

RL J. Biol. Chem. 265:15966-15973(1991).

CC -1- FUNCTION: MAY PLAY A ROLE IN CELL-CELL OR CELL-CYTOKINE
 CC INTERACTIONS DURING THE DEVELOPMENT OF MAST CELLS.

CC -1- SUBCELLULAR LOCATION: Type 2 membrane protein.

CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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CC -----

DR EMBL: M65027; AAA37479.1; .

DR PIR: A40807; A40807.

DR HSSP: P43626; INKP.

DR MCD: XG1:192702; Gp49a.

DR InterPro: IPR007110; IG_1like.

DR PROSITE: PS00635; IG_1like; 1.

KW Signal; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat.

FT SIGNAL 23

FT CHAIN 24 303

FT DOMAIN 24 238

FT TRANSMEM 239 260

FT DOMAIN 261 303

FT DOMAIN 42 125

FT DOMAIN 124 212

FT DISULFID 49 98

FT DISULFID 144 196

FT CARBOHYD 79 79

FT CARBOHYD 133 133

FT CARBOHYD 191 191

FT SEQUENCE 303 AA; 34194 MW; D165659BFA9C40D CRC64;

SC

Query Match

Best Local Similarity 32.4%; Score 289.5; DE 1; Length 303;

Matches 81; Conservative 35; Xismatches 105; Indels 29; Gaps 6;

QY 6 TAFPLGICR-GRVPACSPFLPKPSLCAIPSLVLEKPTLHCQPPGVLLYRLKMS 64

DB 6 TALLVLAATLEERTAVAGHLKPTIWAEPGVIAVTSVLIWQGSWEAGYVTDKXS 65

QY 65 SRYQDAV-----LFIPAKRSLKARTRCSYNGSLWLPSCDLELVATGYFAKS 115

DB 66 VNFMDTEVPLENKKTKRKIRKASVAGIYACVYKSAAGFSEHSDAMELVMTGAVENFS 125

QY 116 ISACGPVAVSSGGDTLCCOTRYGFCQFALYKESDPAPYKPKPK-----YKAS 164

DB 126 LSVYPSRVTSGVSSIFKCSSTLFGRIILIDG-----KQCSKTLDSQVQANPHTAT 186

QY 165 PPIITVTAHSGTYRCYQSSKDPYLWSPFSDPLVYGTSTVPSRLPTLPPSSVAEFS 224

DB 181 FYLDAAVAPNNHGFRCYGFRRNEPQVSKPNSLDLMSEIK-EQSCPTPE--CGLETVQ 237

QY 225 EATAEVTVSF 234

DB 238 KILIGVVSF 247

Search completed: October 23, 2003, 09:42:13

Job time : 27 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: October 23, 2003, 09:35:24 ; Search time 97 seconds

(Method: Alignment)
301.854 Million cell updates/sec

Title: US-09-503-387-3

Perfect score: 1786

Sequence: 1 XSPSPTRAFICGJCGGGRVPA.....XSHQGDGSGQDVHSSRSCS 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 31
Maximum Match 1003
Listing first 45 summaries

Database :
1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mic:*
8: SP_orcellule:*
9: SP_plant:*
10: SP_protist:*
11: SP_virus:*
12: SP_vertebrate:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriophage:*
17: SP_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1786	100.0	339	4	Q9U1F2
2	1676	99.8	321	4	Q9HGN7
3	1555	75.9	620	4	Q9HGN7
4	500	28.0	447	4	Q9HGN7
5	439	27.3	449	4	Q9HGN7
6	438	27.3	449	4	Q9HGN7
7	438	27.3	449	4	Q9HGN7
8	438	27.3	449	4	Q9HGN7
9	438	27.3	449	4	Q9HGN7
10	438	27.3	449	4	Q9HGN7
11	438	27.3	449	4	Q9HGN7
12	438	27.3	449	4	Q9HGN7
13	438	27.3	449	4	Q9HGN7
14	438	27.3	449	4	Q9HGN7
15	438	27.3	449	4	Q9HGN7
16	438	27.3	449	4	Q9HGN7

17	454	25.4	631	4	Q15471
18	449	25.1	631	4	Q15471
19	447.5	25.1	287	4	Q15471
20	443.5	24.8	306	6	Q8Y1Z8
21	443	24.8	307	6	Q8Y1Z8
22	441.5	24.7	466	6	Q8Y1Z8
23	441	24.7	466	6	Q8Y1Z8
24	441	24.7	483	4	Q75022
25	440.5	24.7	306	6	Q95029
26	438.5	24.6	489	4	Q75017
27	436	24.4	305	6	Q8Y1Z8
28	435.5	24.4	305	6	Q8Y1Z8
29	435	24.4	491	4	Q8Y1Z8
30	434	24.3	597	4	Q8Y1Z8
31	434	24.3	598	4	Q8Y1Z8
32	434	24.3	598	4	Q8Y1Z8
33	433	24.2	598	4	Q8Y1Z8
34	429	24.0	590	4	Q75023
35	426.5	23.9	264	6	Q28109
36	425.5	23.8	650	4	Q75024
37	424.5	23.8	643	6	Q8Y1Z8
38	424.5	23.8	662	6	Q8Y1Z8
39	422	23.6	336	6	Q8Y1Z8
40	421.5	23.6	650	4	Q8Y1Z8
41	421.5	23.6	651	4	Q8Y1Z8
42	421.5	23.6	651	4	Q8Y1Z8
43	421.5	23.6	652	4	Q75025
44	416.5	23.3	420	4	Q8Y1Z8
45	416.5	23.3	420	4	Q8Y1Z8

ALIGNMENTS

RESULT 1
Q9U1F2 PRELIMINARY; PRT; 339 AA.
ID Q9U1F2
AC Q9U1F2
DT 01-MAY-2003 (TrEMBLrel. 13, Created)
DT 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
DE Platelet glycoprotein VI precursor (Platelet glycoprotein VI-1).
GN GPVI.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
XP SEQUENCE FROM N.A.
RA Mura Y.;
RT "Platelet glycoprotein VI-1";
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=11027634;
SA Ezumi Y., Chaiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI-1";
RI Eukaryote; Biophys. Res. Commun. 277:27-36(2000).
DR EXBL: AB035073; BA089153.1;
DR EXBL: AB043819; BA01245.1;
DR HSP: F41626.1; NKX;
DR InterPro: IPR03599; IG;
DR InterPro: IPR03006; IG_NHC;
DR Pfam: PF0047; IG_2;
DR SMART: SM00409; IG_2;
KW Signal.
FT SIGNAL 1 20
FT CHAIN 21 339 POTENTIAL;
FT SEQUENCE 339 AA; 36923 MW; 423757695E03CC CRC64;
Query Match 100.0%; Score 1786; DB 4; Length 339;

Best Local Similarity 100.0%, Pred. No. 2,86-146;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

QY 1 MSPPPALFCGLGCGRVPAQSGPLPKPSLQALPSLSVPLEKPYTLRCCGPPGVLYRLE 60
DB 1 MSPPPALFCGLGCGRVPAQSGPLPKPSLQALPSLSVPLEKPYTLRCCGPPGVLYRLE 60
QY 6: KUSSRRYQCAVLEFIPAMKRSLAGRYRCGYNGSLMSLPDQLELVATGVFAKPSLSAQP 122
DB 6: KUSSRRYQCAVLEFIPAMKRSLAGRYRCGYNGSLMSLPDQLELVATGVFAKPSLSAQP 122
QY 12: GRAVSSGGCVTLQCCRYGFFCFALYKBCDPAFYKPEPWIRASPIITVTAAAGCTYRC 180
DB 12: GRAVSSGGCVTLQCCRYGFFCFALYKBCDPAFYKPEPWIRASPIITVTAAAGCTYRC 180
QY 191 YSFSSSDPYLWASPDPLELVYTGTSVPSR--PTSPSSVAEFSATAEIYSEFTNKYRT 240
DB 191 YSFSSSDPYLWASPDPLELVYTGTSVPSRPTPEPSSVAEFSATAEIYSEFTNKYRT 240
QY 241 TETSRITTSPEKSSDPAGAPAQYTKGNVATCGAVILLIAGFLAEDWHSRKRRLRH 300
DB 241 TETSRITTSPEKSSDPAGAPAQYTKGNVATCGAVILLIAGFLAEDWHSRKRRLRH 300
QY 301 RGRAYORPLPPLPQTRKSHGQDGGRCQVHSGSLCS 339
DB 301 RGRAYORPLPPLPQTRKSHGQDGGRCQVHSGSLCS 339

```

RESULT 2

Q9HGN7 PRELIMINARY: PRT: 321 AA.

```

AC Q9HGN7;
DT 01-MAR-2002 (TrEMBLrel. 16, Created)
DT 01-MAR-2002 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Platelet glycoprotein VI 2.
GN GPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OR (1)
RN [1]
RX MEDLINE=20463673; PubMed=11027634;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI."
RL Biochem. Biophys. Res. Commun. 277:36(2000).
DR EMBL AB043823; EMBL2246.1;
DR HSSP: P43626; INKR
DR InterPro: IPR003599; IG
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00347; IG_2.
DR SMART: SMC0409; IG_2.
SC SEQUENCE 321 AA; 35159 MW; 53FBF29945958345 CRC64;

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Query Match 93.8%; Score 1676; D6 4; Length 321;

Best Local Similarity 94.7%; Pred. No. 8,46-137;

```

Matches 331; Conservative 0; Mismatches 0; Indels 18; Gaps 1;
QY 1 MSPPPALFCGLGCGRVPAQSGPLPKPSLQALPSLSVPLEKPYTLRCCGPPGVLYRLE 60
DB 1 MSPPPALFCGLGCGRVPAQSGPLPKPSLQALPSLSVPLEKPYTLRCCGPPGVLYRLE 60
QY 6: KUSSRRYQCAVLEFIPAMKRSLAGRYRCGYNGSLMSLPDQLELVATGVFAKPSLSAQP 120
DB 6: KUSSRRYQCAVLEFIPAMKRSLAGRYRCGYNGSLMSLPDQLELVATGVFAKPSLSAQP 120
QY 12: GRAVSSGGCVTLQCCRYGFFCFALYKBCDPAFYKPEPWIRASPIITVTAAAGCTYRC 180
DB 12: GRAVSSGGCVTLQCCRYGFFCFALYKBCDPAFYKPEPWIRASPIITVTAAAGCTYRC 180
QY 191 YSFSSSDPYLWASPDPLELVYTGTSVPSR--PTSPSSVAEFSATAEIYSEFTNKYRT 240
DB 191 YSFSSSDPYLWASPDPLELVYTGTSVPSRPTPEPSSVAEFSATAEIYSEFTNKYRT 240
QY 241 TETSRITTSPEKSSDPAGAPAQYTKGNVATCGAVILLIAGFLAEDWHSRKRRLRH 300
DB 241 TETSRITTSPEKSSDPAGAPAQYTKGNVATCGAVILLIAGFLAEDWHSRKRRLRH 300
QY 301 RGRAYORPLPPLPQTRKSHGQDGGRCQVHSGSLCS 339
DB 301 RGRAYORPLPPLPQTRKSHGQDGGRCQVHSGSLCS 339

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QY 191 YSFSSSDPYLWASPDPLELVYTGTSVPSR--PTSPSSVAEFSATAEIYSEFTNKYRT 240
DB 191 YSFSSSDPYLWASPDPLELVYTGTSVPSRPTPEPSSVAEFSATAEIYSEFTNKYRT 240
QY 241 TETSRITTSPEKSSDPAGAPAQYTKGNVATCGAVILLIAGFLAEDWHSRKRRLRH 300
DB 241 TETSRITTSPEKSSDPAGAPAQYTKGNVATCGAVILLIAGFLAEDWHSRKRRLRH 300
QY 301 RGRAYORPLPPLPQTRKSHGQDGGRCQVHSGSLCS 339
DB 301 RGRAYORPLPPLPQTRKSHGQDGGRCQVHSGSLCS 339

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RESULT 3

Q9HGN6 PRELIMINARY: PRT: 620 AA.

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AC Q9HGN6;
DT 01-MAR-2002 (TrEMBLrel. 16, Created)
DT 01-MAR-2002 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Platelet glycoprotein VI-3.
GN GPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OR (1)
RN [1]
RX MEDLINE=20463673; PubMed=11027634;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI."
RL Biochem. Biophys. Res. Commun. 277:36(2000).
DR EMBL AB043821; EMBL2247.1;
DR HSSP: P43626; INKR
DR Genes: HGNCL438; GPI6.
DR InterPro: IPR003599; IG
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00347; IG_2.
DR SMART: SMC0409; IG_2.
SC SEQUENCE 620 AA; 67328 MW; FEEB64C5F679615 CRC64;

```

Query Match 95.9%; Score 1355; D6 4; Length 620;

Best Local Similarity 100.0%; Pred. No. 1,26-158;

Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSPPPALFCGLGCGRVPAQSGPLPKPSLQALPSLSVPLEKPYTLRCCGPPGVLYRLE 60
DB 1 MSPPPALFCGLGCGRVPAQSGPLPKPSLQALPSLSVPLEKPYTLRCCGPPGVLYRLE 60
QY 6: KUSSRRYQCAVLEFIPAMKRSLAGRYRCGYNGSLMSLPDQLELVATGVFAKPSLSAQP 120
DB 6: KUSSRRYQCAVLEFIPAMKRSLAGRYRCGYNGSLMSLPDQLELVATGVFAKPSLSAQP 120
QY 12: GRAVSSGGCVTLQCCRYGFFCFALYKBCDPAFYKPEPWIRASPIITVTAAAGCTYRC 180
DB 12: GRAVSSGGCVTLQCCRYGFFCFALYKBCDPAFYKPEPWIRASPIITVTAAAGCTYRC 180
QY 191 YSFSSSDPYLWASPDPLELVYTGTSVPSR--PTSPSSVAEFSATAEIYSEFTNKYRT 240
DB 191 YSFSSSDPYLWASPDPLELVYTGTSVPSRPTPEPSSVAEFSATAEIYSEFTNKYRT 240
QY 241 TETSRITTSPEKSSDPAGAPAQYTKGNVATCGAVILLIAGFLAEDWHSRKRRLRH 300
DB 241 TETSRITTSPEKSSDPAGAPAQYTKGNVATCGAVILLIAGFLAEDWHSRKRRLRH 300
QY 301 RGRAYORPLPPLPQTRKSHGQDGGRCQVHSGSLCS 339
DB 301 RGRAYORPLPPLPQTRKSHGQDGGRCQVHSGSLCS 339

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RESULT 4

Q9HNU6 PRELIMINARY: PRT: 447 AA.

Q9HNU6; DT 01-OCT-2002 (TrEMBLrel. 22, Created)

01-OCT-2002 (Tremblé). 22. Last sequence update;
 01-MAR-2003 (Tremblé). 23. Last annotation update;
 Leukocyte immunoglobulin-like receptor-5.
 LILRB5.
 Homo sapiens (Human).
 CC Eukaryota; Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 CX [1]
 RP SEQUENCE FROM N.A.
 RA Canavog F.C.;
 RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
 DB EMBL: AF283988; AAL36932.1;
 DB InterPro: IPR003066; IG_MHC.
 DR Pfam: PF00047.19; 2.
 SK Receptor.
 SQ SEQUENCE 447 AA; 49193 MW; 6B1E31E2B1C7B14 CRC64;
 Query Match: 28.0%; Score 500; DB 4; Length 447;
 Best Local Similarity 36.0%; Pred. No. 6, 3e-35;
 Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 9;
 QY 1 MSPPTALFCGLCLG-RVPAQSGFLPKPSLQALPSSLVPLEKPYTLRCQTFPGVDYRL 59
 DB 1 MPTTALFCGLSGPRCHWQAGLPKPTLMAEPGSVISKNSVTLKCGTLAEAREYL 60
 QY 60 EKLSRRYQD-----QAVLF-PANKSLAGFRCGSGYNGSJKSPDCLELYATSV 110
 DB 61 EKESPAWDRQNP-LPKKARFSPSTEDYARVRYRSPGWSQSPDFLELYMTGA 120
 QY 111 FAKPSLSAQPGPAGVSSGCVTLCCQTRGCFQGFALYKSGDFAPY-----PARERYRASF 165
 DB 121 YSKPTLSALPSPLVTSKSVTLCCQSRSPKDTFLTKERAAHPLHLKSEHGACQCAEF 180
 QY 166 P1TCTAAHSGTYRCYSFSSRDYLMASAPDPLELYVTGTSVPSRLFTSPSSVAEFSE 225
 DB 191 PMSPTVSVHGTYRCFSHGHSHYLSHPSPLELYVSGSLDEPRSPST----- 229
 QY 226 ATALIVSTNNKVFTESTRITSPKESDPAAGPARYYTKG-----NVRICLGAAY 279
 DB 230 -----RSVSTAAGEPDCQPLPTGSPVPSGLRPMHEVLIGLYVSTL 270
 QY 280 LILLAGF-LAEDMHSRRK-LRKGRAVQRPPLPPLPQTKSHGCGDGGSG----- 330
 DB 271 LLSLLFLQLQHWKQKERTLAQRQADLQRPFGAAEPF-----KDGJQRSSPFAA 322
 QY 331 DVHSRGLCS 339
 DB 323 DVCGENFCA 331
 RESULT 5
 QM1C7 PRELIMINARY; FRT: 448 AA.
 ID 08N1C7.
 AC 08N1C7.
 DT 01-OCT-2002 (Tremblé). 22. Created;
 DT 01-OCT-2002 (Tremblé). 22. Last sequence update;
 DT 01-MAR-2003 (Tremblé). 23. Last annotation update;
 DE Leukocyte immunoglobulin-like receptor, subfamily 5 (with TM and ITIM domains), member 4.
 OS Homo sapiens (Human).
 CC Eukaryota; Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 CX [1]
 RP SEQUENCE FROM N.A.
 RA Straussberg R.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DB EMBL: BC026309; AAH26309.1;
 DB InterPro: IPR003066; IG_MHC.
 DR Pfam: PF00047.19; 2.
 SK Receptor.
 KW

SQ SEQUENCE 448 AA; 49303 MW; A6155D29EFD98912 CRC64;
 Query Match: 27.9%; Score 499; DB 4; Length 448;
 Best Local Similarity 36.0%; Pred. No. 8, 3e-35;
 Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 9;
 QY 1 MSPPTALFCGLCLG-RVPAQSGFLPKPSLQALPSSLVPLEKPYTLRCQTFPGVDYRL 59
 DB 1 MPTTALFCGLSGPRCHWQAGLPKPTLMAEPGSVISKNSVTLKCGTLAEAREYL 60
 QY 60 EKLSRRYQD-----QAVLF-PANKSLAGFRCGSGYNGSJKSPDCLELYATSV 110
 DB 61 EKESPAWDRQNP-LPKKARFSPSTEDYARVRYRSPGWSQSPDFLELYMTGA 120
 QY 111 FAKPSLSAQPGPAGVSSGCVTLCCQTRGCFQGFALYKSGDFAPY-----PARERYRASF 165
 DB 121 YSKPTLSALPSPLVTSKSVTLCCQSRSPKDTFLTKERAAHPLHLKSEHGACQCAEF 180
 QY 166 P1TCTAAHSGTYRCYSFSSRDYLMASAPDPLELYVTGTSVPSRLFTSPSSVAEFSE 225
 DB 191 PMSPTVSVHGTYRCFSHGHSHYLSHPSPLELYVSGSLDEPRSPST----- 229
 QY 226 ATALIVSTNNKVFTESTRITSPKESDPAAGPARYYTKG-----NVRICLGAAY 279
 DB 230 -----RSVSTAAGEPDCQPLPTGSPVPSGLRPMHEVLIGLYVSTL 270
 QY 280 LILLAGF-LAEDMHSRRK-LRKGRAVQRPPLPPLPQTKSHGCGDGGSG----- 330
 DB 271 LLSLLFLQLQHWKQKERTLAQRQADLQRPFGAAEPF-----KDGJQRSSPFAA 322
 QY 331 DVHSRGLCS 339
 DB 323 DVCGENFCA 331
 RESULT 6
 ID 015468 PRELIMINARY; FRT: 448 AA.
 AC 015468.
 DT 01-JAN-1998 (Tremblé). 05. Created;
 DT 01-JAN-1998 (Tremblé). 05. Last sequence update;
 DT 01-MAR-2003 (Tremblé). 23. Last annotation update;
 DE Monocyte inhibitory receptor precursor.
 OS Homo sapiens (Human).
 CC Eukaryota; Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 CX [1]
 RP SEQUENCE FROM N.A.
 RA Arm J.P.; Nwankwo C.; Austen K.F.;
 RL "Molecular identification of a novel family of human immunoglobulin superfamily members that possess immunoreceptor tyrosine-based IT inhibitory motifs and homology to the mouse gp49B1 inhibitory RT receptor".
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DB EMBL: U91925; AAB68665.1; .
 DB HSSP: P45626; INKR.
 DB Genew: HGNC:6608; LILRB4.
 DB InterPro: IPR003599; IG.
 DB InterPro: IPR003066; IG_MHC.
 DR Pfam: PF00047.19; 2.
 DR SMART: SM00459.1; 1.
 KW Receptor; Signal;
 FT SIGNAL 1 23
 FT CHAIN 24 448
 SC SEQUENCE 448 AA; 49297 MW; 7631E24A82EA1399 CRC64;
 Query Match: 27.9%; Score 498; DB 4; Length 448;
 Best Local Similarity 36.0%; Pred. No. 1e-34;
 Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 9;
 QY 1 MSPPTALFCGLCLG-RVPAQSGFLPKPSLQALPSSLVPLEKPYTLRCQTFPGVDYRL 59

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Db 1 MIPFTALLCGLSLGPRTHQAGPLPAPFLMAFGSVYISGNSVTLWCCTLEAREYRL 60
QY 60 EKLSSSRYQD-----QAVLFPAKRSAGRYRSGYONGSLMSPSCLELVATGV 110
Db 61 DKEESPAPWDRQNPLEPKKARFSIPSMTEYAGRYRCYRSPYCWGQSPSPLELVATGA 120
QY 111 FAKPSLSAQPGFANSSGGCVTLCCQTRVGFQFALYKGGAPRY-----KNPEKRYASR 165
Db 121 YKRPFLSALPSPPLVSGKSVTLCCSRPMDTFLIKRAAHFLILHRSRGAQCHAEF 180
QY 166 PIIIVTAASGTYRCYRSPSSRDPYKMSAPSDPLELVATGVTSRPLTPSPSSVAEFS 225
Db 181 FMSPVTSVHGGRYRCFSHGSFSHYLLSHPSDPLELVSGSLGCRPSPT----- 229
QY 226 ATAEIVTFKXVFTTTSRSTTSRKESDSPAARQYVTKG-----NVRICLQAVI 279
Db 233 -----RSVTAAGEEDQPLVPTGSPVPSGSRKRWELIVLVAT 270
QY 280 LIIAGF-LAEDWHSRRK-LRHGRVAVQRPPLPLPQTRKSHGQCGGRQ----- 330
Db 271 LLSLLFLJLQHMWQGRKRLAQGQADFGRRPGAAABEP-----KDGGLCRSSPAA 322
QY 331 DVHSRGLOS 339
Db 323 DVQGENPFA 331

RESULT 7
GENHUS
ID GENHUS PRELIMINARY: PRT: 448 AA.
AC GENHUS:
DT 01-OCT-2002 (Tremblay, 22, Created)
DE 01-OCT-2002 (Tremblay, 22, Last sequence update)
DE 01-MAR-2003 (Tremblay, 23, Last annotation update)
DE Leucocyte immunoglobulin-like receptor 5,
CN LIR-5,
CS Homo sapiens (Human),
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE2335285; Pubmed=12941337;
RA Liu M.R., Kim C., Mwanjoo C., Aschwartz L.K., Ann J.F.;
RT "Genomic organization of the human leucocyte immunoglobulin-like
RT receptors within the leucocyte receptor complex on chromosome
RT 19q34";
RL Immunogenetics 51:659-669(2000);
DR EMBL; AF189768; AAG02024.1;
DR InterPro; IPR033006; I3_MHC;
DR Pfam; PF00047; I3; 2.
DR Receptor.
SQ SEQUENCE 448 AA; 49228 MW; 99310546CEA1393 CRC64;

Query Match 27.9%; Score 498; DB 4; Length 448;
Best Local Similarity 36.0%; Pred. No. 1e-34;
Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 3;

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QY 226 ATAEIVTFKXVFTTTSRSTTSRKESDSPAARQYVTKG-----NVRICLQAVI 279
Db 230 -----RSVTAAGEEDQPLVPTGSPVPSGSRKRWELIVLVAT 270
QY 280 LIIAGF-LAEDWHSRRK-LRHGRVAVQRPPLPLPQTRKSHGQCGGRQ----- 330
Db 271 LLSLLFLJLQHMWQGRKRLAQGQADFGRRPGAAABEP-----KDGGLCRSSPAA 322
QY 331 DVHSRGLOS 339
Db 323 DVQGENPFA 331

RESULT 8
ID 075021 PRELIMINARY: PRT: 448 AA.
AC 075021:
DT 01-NOV-1998 (Tremblay, 08, Created)
DE 01-NOV-1998 (Tremblay, 08, Last sequence update)
DE 01-MAR-2003 (Tremblay, 23, Last annotation update)
DE Leucocyte immunoglobulin-like receptor-5,
CN LIR-5,
CS Homo sapiens (Human),
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Borges L., Hsu M.-L., Fanger N., Kublin M., Cosman D.;
RX Immunology 10:0-0(1997);
DR EMBL; AF028532; AB087666.1;
DR HSSP; P43646; INR;
DR InterPro; IPR003599; I3;
DR InterPro; IPR033006; I3_MHC;
DR Pfam; PF00047; I3; 2.
DR SMART; SMC408; I3; 1.
SQ SEQUENCE 448 AA; 49225 MW; 76D1E07AD3A1399 CRC64;

Query Match 27.9%; Score 498; DB 4; Length 448;
Best Local Similarity 36.0%; Pred. No. 1e-34;
Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 9;

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SEQUENCE FROM N.A.
 STRAIN-FVC;
 RA Berg S.F., Dissen E., Westgaard T.H., Fossum S.;
 PT "Molecular characterization of KIR-1, a novel immunoglobulin-like
 gene in the rat, expressed by NK cells.";
 RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A012741; CA016112;
 DR EMBL: AF025233; AAC69593.1;
 DR HSSP: P43626; INKR.
 DR InterPro: IPR003593; 19;
 DR InterPro: IPR003006; 19_MHC.
 DR Pfam: PF00477; 19; 2.
 DR SMART: SM0409; 19; 2.
 KM Receptor.
 SQ SEQUENCE 325 AA; 37178 MW; 502C10A02F55FA4 CRC64;

Query Match 26.3%; Score 469; DB 11; Length 325;
 Best Local Similarity 37.7%; Pred. No. 2,1e-32;
 Matches 115; Conservative 36; Mismatches 126; Indels 36; Gaps 5;

1 MSPTPALFCGLG-RVPAQSGFLPSPICAPSPSLVPLEKPYTLACQSPGVDIYR-39
 1 KPTITLALGGLGSGRIINERKCLPRTIWAQSIWTKGNVHWCQAGASRQL-60
 59 -----LKKSSRRDQALFTPAKRSIAGRCYQNSMSLPSCLEVALTV-110
 61 YEGSPFALERKSRKSKKVFETISQTSHTAG-YTCFYSGELMSSSNPALVYVTL-120
 111 FAKPSLSAQPGFVSSGCVTLQCTRYGQCPALYKEDPAVYNGRWRASFPITVY-170
 121 YPTFLVHPGPEVLCENVTSCHLKATSKFELKRRSHIOHKYKNCLETFMGPV-180
 171 TAAISGTRCYFSFSDPYLWASADPPELVYTCISVTPSRIPTEPSSVA--EFSEKTA-228
 191 TPANRGIVRC--FGSYNYAMSPSPSPVTLITCEVENTS-LPTNPVSSLYWEFEST-237
 223 ETVSFTKVFETTSFSTTPKESCSAPAGAYYKKNVETCGAVNLITAGSLA-248
 238 -----KESGQKCSAFKCNHAKNLLIRGLKGLVWMLVWICL-274

DB 289 EDWHSRRK 296
 275 EDWHSRRK 282

RESULT 12
 08NMJ23 PRELIMINARY; PRT; 631 AA.
 AC 08NMJ23;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Leukocyte immunoglobulin-like receptor d.
 GN LIR.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Pan.
 CX NCBI_TaxID=9598;
 RN 1;
 RS SEQUENCE FROM N.A.
 RX MEDLINE=2155186; PubMed=1169452;
 RA Caravez F.C., Young N.T., Gethlein L.A., Rajalingam R., Khakoo S.I.,
 RA Shum B.P., Parham P.;
 RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes
 RT reveals a framework and rapidly evolving genes.";
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF383168; AL31871.1;
 DR InterPro: IPR003593; 19;
 DR InterPro: IPR007113; 19-like.
 DR InterPro: IPR003588; 19_C2.
 DR InterPro: IPR033066; 19_MHC.
 DR Pfam: PF00477; 19; 4.
 DR SMART: SM00409; 19; 4.

DR SMART: SM0408; 19C2; 2.
 DR PROSITE: PS00835; IG_LIKE; 2.
 KM Immunoglobulin domain; Receptor.
 SQ SEQUENCE 631 AA; 69456 MW; 10E3706D3B4D6FF CRC64;

Query Match 26.3%; Score 464; DB 6; Length 631;
 Best Local Similarity 39.5%; Pred. No. 1.4e-31;
 Matches 133; Conservative 46; Mismatches 107; Indels 20; Gaps 7;

1 MSPTPALFCGLG-RVPAQSGFLPSPICAPSPSLVPLEKPYTLACQSPGVDIYR-59
 1 KPTITLALGGLGSLGPRHVQAGFLPTLAEQSV--RSPPTTKQGNLSAEVCL-60
 60 EKSSRRYCD-----CAVFTPAKRSIAGRCYQNSMSLPSCLEVALTV-110
 61 YEGSPFALERKSRKSKKVFETISQTSHTAG-YTCFYSGELMSSSNPALVYVTL-120
 111 FAKPSLSAQPGFVSSGCVTLQCTRYGQCPALYKEDPAVYNGRWRASFPITVY-170
 121 YPTFLVHPGPEVLCENVTSCHLKATSKFELKRRSHIOHKYKNCLETFMGPV-180
 171 TAAISGTRCYFSFSDPYLWASADPPELVYTCISVTPSRIPTEPSSVAEFS-224
 181 FPGVPTSHRMTFRVYVYVNDQWMSRSPPLILSGVSRKSLITLQSP-VLAGEE-239
 225 EATVEL--TVSFTKVFETTSFSTTPKESCSAPAGAYYKKNVETCGAVNLITAG-268
 240 SLTLQCSQDYGDFLYKESGRDPLORPQCPQ-AGLSQANFTLG-284

DB 240 SLTLQCSQDYGDFLYKESGRDPLORPQCPQ-AGLSQANFTLG-284

RESULT 13
 076036 PRELIMINARY; PRT; 304 AA.
 ID 076036;
 AC 076036;
 DT C-NOV-1998 (TREMBLrel. 08, Created)
 DT C-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT C-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE NK receptor (lymphocyte antigen 94 homolog, activating NK-receptor,
 DE NK-p46) (Ncuse).
 GN NK-P46.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN 1;
 RS SEQUENCE FROM N.A.
 RC T-SUE=Lymphoid;
 RX MEDLINE=58401029; PubMed=9770896;
 RA Persing A., Sivori S., Bollino G., Malaspina A., Morelli L.,
 RA Moretta L., Bissocci R., Vignetti A.;
 RT "Molecular cloning of NKp46, a novel member of the immunoglobulin
 RT superfamily involved in triggering of natural cytotoxicity.";
 RU J. Exp. Med. 188:953-960(1998).
 RN 1;
 RS SEQUENCE FROM N.A.
 RC T-SUE=Blood;
 RA Strauszberg R.;
 RU Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC03193; CAAC0474.1;
 DR EMBL: BC030265; AAH30265.1;
 DR HSSP: P43626; INKR.
 DR Gene: HNGC:6731; NCRL.
 DR InterPro: IPR003006; 19_MHC.
 DR Pfam: PF00477; 19; 2.
 KM Receptor.
 SQ SEQUENCE 304 AA; 34480 MW; FBCBDE50D2F34CD3 CRC64;

Query Match 25.7%; Score 459; DB 4; Length 304;
 Best Local Similarity 36.1%; Pred. No. 1.4e-31;
 Matches 117; Conservative 45; Mismatches 108; Indels 54; Gaps 9;

1 MSPTPALFCGLG-RVPAQSGFLPSPICAPSPSLVPLEKPYTLACQSPGVDIYR-59
 1 KPTITLALGGLGSLGPRHVQAGFLPTLAEQSV--RSPPTTKQGNLSAEVCL-60

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DB 1 MASTPALLCGLGCLISQR:SAQQQLFKPFIMWAPHEFMVREKQVY:CCQGNAGVEXOL 60
CY 60 -----EKSSSSRYQDAVLP:TPANKRSILAK:RRCQYQNGSLNS:PPSOOL 164
DB 61 HPESSILFAVDRPKFPRKRNKYF:-----Y:PDMSNMAGQYSC:YVAGELMSFESS:LD 114
CY 105 IYATGVFAKPS:SAQPGPAVSSGCVTLQCCQRYGFPDPA:YKESDPAFYNPRMWPAS 164
DB 115 LVTVMYDPTFLSVHPGFEV:SGEKVTFYCRJDTN:SVPLIKERSSHVOCR3:GKXCAE 174
CY 165 PFIIVTAHSGTYP:CVAFSSRRDPY:KASPSDELAVYTG:-----TSVTPSSNUTPPSSV 220
DB 175 PFLGVTJAHRTYRC:FGSYNNHWSFSPSEPVTLV:GDIENSLAFED:PPFPATY 231
CY 221 AEFSEATHELTYSFNKYFTTETSRS:TTSPRESSDPAGPRQYTKNLVYICL:AVIL 290
DB 232 GTY:-----L:LTETG:-----LCKDH:-----LMDSTACNL:RXYGLAFYVL 266
CY 251 ITLAGFLADKMSRPRK:LRHGR 304
DB 267 VAVYVFLVYEDWLSRKRTRERASRA 290

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RESULT 14

032004

ID 092004 PRELIMINARY: PR7: 325 AA.

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AC 092004: 01-MAY-1999 (Tremblrel, 10, Created)
AT 01-MAY-1999 (Tremblrel, 10, Last sequence update)
DT 01-MAR-2003 (Tremblrel, 23, Last annotation update)
DE Activating receptor 1.
NCBI OR 1994 OR MAR-1.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=99193527; PubMed=10092106;
RA Blasson R., Bessino A., Bostino C., Bende D., Xoretta L., Xoretta A.;
RT "The murine homologue of the human KIR46, a triggering receptor
RT involved in the induction of natural cytotoxicity."
RL Eur. J. Immunol. 29:1014-1020(1999).
DR EMBL: A229765; CAB39169.1;
DR HSPB; P43626; INKR.
DR XGN; XGI:136212; Ncrl.
DR InterPro: IPR003599; I9.
DR InterPro: IPR003006; I9_YHC.
DR Pfam: PF00347; I9; 2.
DR SMART: SMC0400; I9; 2.
SK Receptor.
SQ SEQUENCE 325 AA; 37265 MW; ED24E46ABF22C29 CRC64;

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Query Match

Best Local Similarity 38.0%; Score 459; DB 11; Length 325;
Matches 117; Conservative 36; Mismatches 117; Indels 38; Gaps 6;

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CY 1 MSPPTALFCGLGCLG-RVPAQSGP:PKPSLQALPSSLYPEKPYTLRCQGPFGVLYR 58
DB 1 MPTPTALFCGLGCLISQR:INTEKTLPKPIIAKPSIYNWNGNSVNIWQGASASEYOL 60
CY 59 -----LEKSSSRVQDAVLP:TPANKRSILAK:RRCQYQNGSLNS:PPSOOL 164
DB 61 HPESSILFAVDRPKFPRKRNKYF:-----Y:PDMSNMAGQYSC:YVAGELMSFESS:LD 114
CY 111 FAKPSLSAOPGPAVSSGCVTLQCCQRYGFPDPA:YKESDPAFYNPRMWPASFP:ITV 170
DB 121 VOTKMLWYVPPREVTLGENVTFCCQKATKSKF:LLKRGSHIOMKXGN:CAEPFPGPV 160
CY 171 TAAHSGTYRCYFSSSDPYLNASPDPELVYTG:SVTPSR:LTSPSSVA--EPESEATA 223
DB 181 TAAHRTYRC--FGSYNNHWSFSPSEPVTL:ITGVENSS:LAFTDPTSSLDWEPFLSTN 238
CY 181 TAAHRTYRC--FGSYNNHWSFSPSEPVTL:ITGVENSS:LAFTDPTSSLDWEPFLSTN 238

```

```

CY 229 ELYVSPFNKYFTTETSRS:TTSPKESDPAFAGARQYTKRN:VRIQLGAVILIIAGFLA 268
DB 239 E-----SGLQKDS-----AFWDHTON:IRIGLACI:LTITLWDEL 274
CY 289 EDHRSRK 296
DB 275 EDWLSRK 282

```

RESULT 15

03C967

ID 03C967 PRELIMINARY: PR7: 325 AA.

```

AC 03C967: 01-MAR-2003 (Tremblrel, 23, Created)
AT 01-MAR-2003 (Tremblrel, 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel, 23, Last annotation update)
DE Lymphocyte antigen 94.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C37BL/6J; TISSUE=Bone;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL: AK079431; BAC37635.1;
SQ SEQUENCE 325 AA; 37237 MW; 42272A976B3B3F34 CRC64;

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Query Match

Best Local Similarity 38.0%; Score 459; DB 11; Length 325;
Matches 117; Conservative 36; Mismatches 117; Indels 38; Gaps 6;

```

CY 1 MSPPTALFCGLGCLG-RVPAQSGP:PKPSLQALPSSLYPEKPYTLRCQGPFGVLYR 58
DB 1 MPTPTALFCGLGCLISQR:INTEKTLPKPIIAKPSIYNWNGNSVNIWQGASASEYOL 60
CY 59 -----LEKSSSRVQDAVLP:TPANKRSILAK:RRCQYQNGSLNS:PPSOOL 164
DB 61 HPESSILFAVDRPKFPRKRNKYF:-----Y:PDMSNMAGQYSC:YVAGELMSFESS:LD 114
CY 111 FAKPSLSAOPGPAVSSGCVTLQCCQRYGFPDPA:YKESDPAFYNPRMWPASFP:ITV 170
DB 121 VOTKMLWYVPPREVTLGENVTFCCQKATKSKF:LLKRGSHIOMKXGN:CAEPFPGPV 160
CY 171 TAAHSGTYRCYFSSSDPYLNASPDPELVYTG:SVTPSR:LTSPSSVA--EPESEATA 223
DB 181 TAAHRTYRC--FGSYNNHWSFSPSEPVTL:ITGVENSS:LAFTDPTSSLDWEPFLSTN 238
CY 229 ELYVSPFNKYFTTETSRS:TTSPKESDPAFAGARQYTKRN:VRIQLGAVILIIAGFLA 268
DB 239 E-----SGLQKDS-----AFWDHTON:IRIGLACI:LTITLWDEL 274
CY 289 EDHRSRK 296
DB 275 EDWLSRK 282

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Search completed: October 23, 2003, 09:40:15
Job time : 103 secs

GenScan version 5.1.6
Copyright (c) 1992 - 2003 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: October 23, 2003, 09:32:24 Search time 23 seconds

without alignment 648,253 million cell updates/sec

Title: US-09-503-387-3

Perfect score: 1786

Sequence: 1 MSPSPALPFCGLCLGRVPA.....KSHGCGCGRQVHSRLCS 333

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 5
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

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24: /S:SDSI/gcgdata/geneseq/geneseq-emb1/AA1973.DAT.*
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Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1786	100.0	339	22	HUMAN TANGO 268 pr
2	1786	100.0	339	24	ABU11221
3	1782	99.8	339	22	HUMAN TANGO 268 pr
4	1782	99.8	339	22	ABAB1274
5	1782	99.8	339	22	ABAB1275
6	1782	99.8	339	22	ABAB1276
7	1782	99.8	339	24	ABU11239
8	1782	99.8	339	24	ABU11240
9	1782	99.8	339	24	ABU11241

10	1782	99.8	339	24	ABU11242
11	1770	99.1	339	22	ABAB1269
12	1759	98.6	339	22	ABU12793
13	1678	94.0	339	22	ABAB1257
14	1678	94.0	339	22	ABAB1258
15	1678	94.0	339	24	ABU11223
16	1331	73.4	501	24	ABU12815
17	1327.5	73.2	502	24	ABU12819
18	1304	73.0	249	22	ABAB1261
19	1304	73.0	249	24	ABU11227
20	1304	73.0	359	22	ABU12791
21	1122	62.8	333	22	ABAB1265
22	1122	62.8	333	22	ABAB1266
23	1122	62.8	333	24	ABU11231
24	1122	62.8	333	24	ABU11245
25	1118	62.6	333	22	ABAB1277
26	1118	62.6	333	22	ABAB1278
27	1118	62.6	333	22	ABAB1279
28	1118	62.6	333	24	ABU11243
29	1118	62.6	333	24	ABU11244
30	1118	62.6	333	24	ABU11245
31	1080.5	60.5	232	22	ABAB1267
32	1080.5	60.5	232	22	ABU11233
33	1078	60.4	233	23	ABU12866
34	937	52.5	257	22	ABAB1268
35	937	52.5	257	24	ABU11234
36	498	27.9	448	13	ABAB1251
37	498	27.9	448	19	ABAB1263
38	498	27.9	448	21	ABAB1264
39	492	27.5	472	13	ABAB1265
40	491	27.5	447	24	ABU12940
41	477	26.7	289	13	ABAB1248
42	477	26.7	289	21	ABAB1249
43	457	25.6	632	24	ABU12086
44	455	25.5	299	21	ABAB1280
45	455	25.5	299	22	ABU12330

ALIGNMENTS

RESULT 1	ABAB1255
10	ABAB1255 standard; Protein; 339 AA.
AC	ABAB1255:
XX	
04-APR-2001 (first entry)	
XX	
DE	HUMAN TANGO 268 protein.
XX	
KW	Human; TANGO 268; cardiac; cerebroprotective; cytoprotective; anticoagulant;
KW	truncoblytic; anti-arteriosclerotic; haemostatic; glycoprotein VI; GPIIb/
KW	platelet membrane glycoprotein receptor; bleeding disorder;
KW	blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW	ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW	cancer.
XX	
OS	Homo sapiens.
XX	
FN	W0200102810-01.
PD	04-JAN-2001.
XX	
PF	30-JUN-2000; 2000NC-0518152.
XX	
PR	30-JUN-1999; 98US-0345468.
PR	06-DEC-1993; 98US-0454824.
PR	14-FEB-2000; 2000US-0503867.
XX	
PA	(MILL-1) MILLENNIUM PHARM INC.
XX	
PI	Bufffield St. Villela J. Candrot-Fernus W. Valinchenker W. Gill DS;

Glycoprotein VI as
Amino acid sequenc
Human platelet me-
Mature human TANGO
Human Glycoprotein
Human TANGO 268 aa
Immunoglobulin FC-
Glycoprotein VI-
Human TANGO 268 ex
Human TANGO 268 ex
Human GPIIb externa
Mouse TANGO 268 pr
Mouse TANGO 268 pr
Mouse TANGO 268 pr
Glycoprotein VI as
Glycoprotein VI as
Mouse TANGO 268-re
Mouse TANGO 268-re
Mouse TANGO 268-re
Glycoprotein VI as
Glycoprotein VI as
Glycoprotein VI as
Mature mouse TANGO
Mouse TANGO 268 pr
Human platelet gly
Mouse TANGO 268 ex
Mouse TANGO 268 pr
Human LIR-ph2 fro
Human gp49 Hm.8 po
Leukocyte immunog.
FCR-IV protein seq
Human GENSFT polyp
Human LIR-ph2-2
Leukocyte immunog
Human NOV27a CG938
Leukocyte immunog
Human TANGO 5.1 am

21 Qian WD, Kingsbury G;
 XX WPI: 2001-080877/09.
 DR N-2SDB: AAF2947C, AAF2947L.
 XX
 XX New genes encoding human platelet-expressed collagen receptor,
 PT glycoprotein VI, and its modulators, useful for preventing, treating
 PT and diagnosing hemostatic disorders, thrombotic diseases and
 XX immunological disorders -
 XX
 PS Claim 8: Fig 1A: 227pp; English.
 XX
 CC The present sequence is given in a specification relating to an isolated
 CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
 CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
 CC and polypeptides and their modulators, e.g. antisense nucleic acids,
 CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders
 CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
 CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
 CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
 CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
 CC infarction), immunological diseases (e.g. platelet disorders) and
 CC embryonic liver disorders. Preferably they are used to prevent acute
 CC cardiac ischaemia following angioplasty and retarctatic cancers,
 CC especially of the colon and liver.
 CC
 SC Sequence 339 AA;
 Query Match 100.0%; Score 1786; DB 24; Length 339;
 Best Local Similarity 100.0%; Pred. No. 6.2e-141;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSFSPALPCLGCLGRVPAQSGPLPKPSLQALPSSLVLEKPYTLRCGPGVLDYRLE 60
 DB 1 MSFSPALPCLGCLGRVPAQSGPLPKPSLQALPSSLVLEKPYTLRCGPGVLDYRLE 60
 QY 61 KSSSSYYDOANLFTPAKRSAGAVRCQYQYQNSNSPSDQLELVAGVPAKPSLNSQP 120
 DB 61 KSSSSYYDOANLFTPAKRSAGAVRCQYQYQNSNSPSDQLELVAGVPAKPSLNSQP 120
 QY 121 GAVSSGQSVTLCCQTPYQFQFALYKESQDPAPYKQPPFVYASPTITVYANSSTYRC 180
 DB 121 GAVSSGQSVTLCCQTPYQFQFALYKESQDPAPYKQPPFVYASPTITVYANSSTYRC 180
 QY 131 YPSSSTPYLWASDPDLNVTYTSYTPSPFLTPSPSSVYEFSSALDELTVSFTNKYFT 240
 DB 131 YPSSSTPYLWASDPDLNVTYTSYTPSPFLTPSPSSVYEFSSALDELTVSFTNKYFT 240
 QY 241 TTSRSITTSPEKSSSPAFAPQYTKQVNLICGAVYLITLAEFLDEKHSRKRRLH 300
 DB 241 TTSRSITTSPEKSSSPAFAPQYTKQVNLICGAVYLITLAEFLDEKHSRKRRLH 300
 QY 301 RGRAVQRPPLPPLPPLPQTKRSHSGQDGRDYSRGLCS 339
 DB 301 RGRAVQRPPLPPLPPLPQTKRSHSGQDGRDYSRGLCS 339
 RESULT 2
 ABU11221
 ID ABU11221 standard; Protein: 339 AA.
 XX
 AC ABU11221;
 XX
 XX 06-FEB-2003 (first entry)
 XX
 DE Human TANGO 268 protein.
 XX
 KW Human; mouse; variable heavy; VH; antigen: cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW Proliferation; migration; embryogenesis; inflammation; thrombosis;

KW degradation; thrombocytopaenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.
 XX
 OS Homo sapiens.
 XX
 PR NC002080968-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 09-APR-2002; 2002WC-0511122.
 XX
 PR 09-APR-2001; 2001CS-0829495.
 XX
 FA (MILL.) WILLENITOX PHARM INC.
 XX
 F1 Basfield SC, Villaval C, Jandrot-Perrus M, Vainchencker W, Gill DS;
 P1 Qian WM, Kingsbury G;
 XX
 XX WPI: 2001-080877/09.
 DR N-2SDB: AAF2947C, AAF2947L.
 XX
 PT Novel substantially purified antibody immunospecifically binding to
 PT TANGO 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopaenia, stroke, ischaemia, pulmonary embolism, atherosclerosis
 PT -
 PS Disclosure: Figure 1; 23pp; English.
 XX
 CC This invention relates to a novel purified antibody comprising a
 CC variable heavy (VH) complementarity determining region (CDR1, VH CDR2
 CC or VH CDR3) or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
 CC immunospecifically binding to a TANGO 268 (also referred as glycoprotein
 CC VI (GPVI)) antigen. The antibodies of the invention act to decrease or
 CC block TANGO 268 binding to extracellular matrix components, or as a
 CC collagen or platelet release and aggregation blocker. The antibodies of
 CC the invention are useful for modulating proliferation, migration,
 CC angiogenesis, differentiation and/or function of megakaryocytes and
 CC platelets, including during development e.g. embryogenesis, modulating
 CC leucocyte-platelet and platelet-endothelium interactions in
 CC inflammation and/or thrombosis, and modulating platelet aggregation and
 CC degradation. They are also useful for modulating disorders associated
 CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
 CC migration, morphology, differentiation and/or function, e.g. bleeding
 CC disorders such as thrombocytopaenia. Other diseases which may be
 CC modulated by these antibodies are thrombotic disorders, cerebral
 CC vascular diseases (e.g. stroke and ischaemia), venous thromboembolism
 CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
 CC pulmonary embolism, etc), coronary diseases (e.g. cardiovascular
 CC diseases including angina pectoris, myocardial infarction, coronary
 CC restenosis, atherosclerosis, etc), immunological disorders,
 CC developmental disorders, embryonic disorders, liver disorders, cerebral
 CC vascular diseases, venous thromboembolism disease, coronary diseases,
 CC and metastatic cancers. The antibodies of the invention only causes a
 CC transient decrease in platelet counts, platelet aggregation, and/or
 CC platelet activation and so have some advantages over prior art
 CC methods. The present sequence represents a protein sequence used to
 CC create the antibodies of the invention.
 CC
 SC Sequence 339 AA;
 Query Match 100.0%; Score 1786; DB 24; Length 339;
 Best Local Similarity 100.0%; Pred. No. 6.2e-141;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSFSPALPCLGCLGRVPAQSGPLPKPSLQALPSSLVLEKPYTLRCGPGVLDYRLE 60
 DB 1 MSFSPALPCLGCLGRVPAQSGPLPKPSLQALPSSLVLEKPYTLRCGPGVLDYRLE 60

2Y KSSRYQDQAVLFIIPAKRSLAGRYCSYNGSLMSPLDQLCVATGVFAKSLSAQF 120
 CC |||||
 CC KSSRYQDQAVLFIIPAKRSLAGRYCSYNGSLMSPLDQLCVATGVFAKSLSAQF 120
 CC |||||
 CC 61 KSSRYQDQAVLFIIPAKRSLAGRYCSYNGSLMSPLDQLCVATGVFAKSLSAQF 120
 CC |||||
 CC 121 GPVSSGGCVTLQCTRTGDFOPALYKSGDPAPYKNEPRWYAFPIITVTAHSGTYRC 180
 CC |||||
 CC 122 GPVSSGGCVTLQCTRTGDFOPALYKSGDPAPYKNEPRWYAFPIITVTAHSGTYRC 180
 CC |||||
 CC 181 YSFSSRDFYLMGASDPLFLVVTGTSVTFSSLFTEPPSSVAEPSEATAEITVSTNYVFT 240
 CC |||||
 CC 182 YSFSSRDFYLMGASDPLFLVVTGTSVTFSSLFTEPPSSVAEPSEATAEITVSTNYVFT 240
 CC |||||
 CC 241 TETSRITTSPEKSDSPAGPAPQYTKNIVKICIGAVLILLAGFLAEKHSRRKRLRH 300
 CC |||||
 CC 242 TETSRITTSPEKSDSPAGPAPQYTKNIVKICIGAVLILLAGFLAEKHSRRKRLRH 300
 CC |||||
 CC 301 RGAAYGRPLPPLPCTRKSHSGDGGGRQDVHSGGLCS 339
 CC |||||
 CC 302 RGAAYGRPLPPLPCTRKSHSGDGGGRQDVHSGGLCS 339
 CC |||||

RESULT 3

AAB6:273
 ID AAB6:273 standard; Protein; 339 AA.
 XX
 AC AAB6:273;

04-APR-2001 (first entry)

Human TANGO 268-related protein #1.

Human; TANGO 268; cardiact; cerebroprotective; cytosstatic; anticoagulant;
 thrombolytic; antiatherosclerotic; haemostatic; glycoprotein VI; GPIIb;
 platelet membrane glycoprotein receptor; bleeding disorder;
 blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 ischaemia; cardiovascular disease; immunological disease; liver disorder;
 cancer.

Homo sapiens.
 MO200100810-A1.
 04-JAN-2001.
 30-JUN-2003; 2000NC-05:8152.
 30-JUN-1999; 99US-0345468.
 06-DEC-1999; 99US-0454824.
 14-FEB-2000; 2000US-0503187.
 (MILL-) WILBENITON PHARM INC.
 Busfield SJ, Vilella J, Jandrot-Perrus M, Vainchenker W, Gill DS;
 Qian MD, Kingsbury G;
 WPI: 2001-060877/09.
 K-PSDB; AAF29484.

New genes encoding human platelet-expressed collagen receptor,
 glycoprotein VI, and its modulators, useful for preventing, treating
 and diagnosing hemorrhagic disorders, thrombotic diseases and
 immunological disorders.

Disclosures: Page 213-214; 227pp; English.

The present sequence is given in a specification relating to an isolated
 nucleic acid molecule encoding a platelet membrane glycoprotein receptor
 glycoprotein VI (GPIIb), also called TANGO 268. The GPIIb polynucleotides
 and polypeptides and their modulators, e.g. antithrombotic agents,
 fibrinolytics and antibodies, are useful for preventing, treating and
 diagnosing disorders associated with aberrant expression or activity of
 GPIIb. These disorders include bleeding disorders
 (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders

CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
 disorders, coronary artery and cerebral artery diseases (e.g. stroke and
 ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
 infarction), immunological diseases (e.g. platelet disorder) and
 embryonic liver disorders. Preferably they are used to prevent acute
 cardiac ischaemia following angioplasty and metastatic cancers,
 especially of the colon and liver.

Sequence 339 AA;

Query Match 99.8%; Score 1782; DB 22; Length 339;

Best Local Similarity 99.7%; Pred. No. 13e-140;

Matches 338; Conservative 0; X-matches 2; Indels 0; Gaps 0;

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 CC |||||
 CC 122 GPVSSGGCVTLQCTRTGDFOPALYKSGDPAPYKNEPRWYAFPIITVTAHSGTYRC 180
 CC |||||
 CC 61 KSSRYQDQAVLFIIPAKRSLAGRYCSYNGSLMSPLDQLCVATGVFAKSLSAQF 120
 CC |||||
 CC 62 KSSRYQDQAVLFIIPAKRSLAGRYCSYNGSLMSPLDQLCVATGVFAKSLSAQF 120
 CC |||||
 CC 181 YSFSSRDFYLMGASDPLFLVVTGTSVTFSSLFTEPPSSVAEPSEATAEITVSTNYVFT 240
 CC |||||
 CC 182 YSFSSRDFYLMGASDPLFLVVTGTSVTFSSLFTEPPSSVAEPSEATAEITVSTNYVFT 240
 CC |||||
 CC 241 TETSRITTSPEKSDSPAGPAPQYTKNIVKICIGAVLILLAGFLAEKHSRRKRLRH 300
 CC |||||
 CC 242 TETSRITTSPEKSDSPAGPAPQYTKNIVKICIGAVLILLAGFLAEKHSRRKRLRH 300
 CC |||||
 CC 301 RGAAYGRPLPPLPCTRKSHSGDGGGRQDVHSGGLCS 339
 CC |||||
 CC 302 RGAAYGRPLPPLPCTRKSHSGDGGGRQDVHSGGLCS 339
 CC |||||

RESULT 4

AAB6:274
 ID AAB6:274 standard; Protein; 339 AA.
 XX
 AC AAB6:274;

04-APR-2001 (first entry)

Human TANGO 268-related protein #2.

Human; TANGO 268; cardiact; cerebroprotective; cytosstatic; anticoagulant;
 thrombolytic; antiatherosclerotic; haemostatic; glycoprotein VI; GPIIb;
 platelet membrane glycoprotein receptor; bleeding disorder;
 blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 ischaemia; cardiovascular disease; immunological disease; liver disorder;
 cancer.

Homo sapiens.

MO200100810-A1.

04-JAN-2001.

30-JUN-2003; 2000NC-05:8152.

30-JUN-1999; 99US-0345468.

06-DEC-1999; 99US-0454824.

14-FEB-2000; 2000US-0503187.

(MILL-) WILBENITON PHARM INC.

Busfield SJ, Vilella J, Jandrot-Perrus M, Vainchenker W, Gill DS;
 Qian MD, Kingsbury G;


```

RESULT 6
AA061276
ID   AA061276 standard; Protein; 339 AA.
XX
XX
XX AC   AAB61276:
XX CT   04-APR-2001 (first entry)
XX DE   Human TAWGC 268-related protein #4.
XX
XX   Human: TAWGC 268-related protein #4.
XX KW   Human; TAWGC 268; cartilage; cerebroprotective; cytosolic; anticoagulant;
XX KW   thrombinolytic; antiarteriosclerotic; hemostatic; glycoprotein VI; GPII;
XX KW   platelet membrane glycoprotein receptor; bleeding disorder;
XX KW   blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
XX KW   ischaemia; cardiovascular disease; immunological disease; liver disorder;
XX KW   cancer.
XX
XX   Homo sapiens.
XX OS
XX FN   WO2001002810-A1.
XX PD   04-JAN-2001.
XX PF   30-JUN-2000; 2000WG-US15152.
XX PR   30-JUN-1999; 59US-0345468.
XX PR   26-DEC-1999; 59US-0454824.
XX PR   14-FEB-2000; 2000US-0503387.
XX
XX   (MILL.) MILLENNIUM PHARM INC.
XX PA
XX   Busefield SJ, Vajjala C, Jandrot-Perrus M, Valchenkov W, Gitt DS;
XX   Qian XD, Kirgibayev G;
XX DR   NPSIDE; AAP29487.
XX
XX   New genes encoding human platelet-expressed collagen receptor,
XX PT   glycoprotein VI, and its modulators, useful for preventing, treating
XX PT   and diagnosing hemorrhagic disorders, thrombotic diseases and
XX PT   immunological disorders -
XX PS
XX   Disclosure: Page 217; 227pp; English.
XX
XX   The present sequence is given in a specification relating to an isolated
XX CC   nucleic acid molecule encoding a platelet membrane glycoprotein receptor
XX CC   glycoprotein VI (GPII), also called TAWGC 268. The GPII polynucleotides
XX CC   and polypeptides and their modulators, e.g. antisense nucleic acids,
XX CC   ribozymes and antibodies, are useful for preventing, treating and
XX CC   diagnosing disorders associated with aberrant expression or activity of
XX CC   GPII. These disorders include bleeding disorders
XX CC   (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
XX CC   (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
XX CC   disorders, coronary artery and cerebral artery diseases (e.g. stroke and
XX CC   ischaemia), cardiovascular diseases (e.g. arteriosclerosis and "vascular
XX CC   interaction"), immunological diseases (e.g. platelet disorder) and
XX CC   embryonic liver disorders. Preferably they are used to prevent acute
XX CC   cardiac ischaemia following angioplasty and metastatic cancers,
XX CC   especially of the colon and liver.
XX
XX   Sequence      339 AA:
XX
Query Match:          99.8%; Score 1792; DS 22; Length 339;
Best Local Similarity 99.7%; PEG. No. 13e-140;
Matches 335; Conservative 0; Mismatches 1; Indels 0; Caps 0
Y
1 MSPSPARFELGLCLGRVACAGSPKPKPLQCLPESLYPEAKPTLRCGGPGGVAVRLS 60
Dp : MSRSPTLLFLGLSLGRVPAAGGPAPKPSQLPLSSVPLLPKPTLRCCGPGGVAVRLS 60
Y KLSRRSQCVAVLFIPMKRSLAGRVCYONGSLWSLPSQDLVAIVGFAXNDJSGNP 120

```

D6		61	KASSSSQYQDAVLFPZMKESLAGVPSSEYNOSLWSLPSCDLPLVATGVFAKPSLSACP	127
D7		121	GPAVSAGGAVTLCCOIRKGPDPGFALFKRGCDAPFKNPFRWRASFPSTTTAASGTIRC	189
D8		121	GPVSSGGGVTLQCQRIRGPDGFALKKGADAFPKNBRWRASFPTTTAAHSGTIRC	189
D9		181	VSPSRSDPLPMASPEDFLELVYTGTVTPSGLDTEPRSSVAEFSERAEITVFSTNKCVFT	247
D9		181	VSPSRSDPLPMASPEDFLELVYTGTVTPSGLDTEPRSSVAEFSERAEITVFSTNKCVFT	247
D9		241	TETSSRSLTTSPPKSSSSPGAPARCYTKCNLVRCIGAYILLIILAGFLAEDMHSRKRLRH	300
D9		241	TETSSRSLTTSPPKSSSSPGAPARCYTKCNLVRCIGAYILLIILAGFLAEDMHSRKRLRH	300
D9		301	RGRNVORPLPLPLPCTCRKSHGGGCCDCRRCDVHRSGCS	339
D9		301	RGRNVORPLPLPLPCTCRKSHGGGCCDCRRCDVHRSGCS	339
RESULT 7				
AEU11238		ID	ABJ11239 standard: Protein; 339 AA.	
AC		AC	ABJ11239;	
C7		C7	06-FEB-2003 (first entry)	
DE		DE	Glycoprotein VI associated protein sequence #1.	
XX		XX	Human; mouse; variable heavy; VH; antigen; cancer;	
KW		KW	complementarity determining region; TANGO 268; glycoprotein VI; GPeVI;	
KM		KM	TANGO 268; extracellular matrix; collagen; platelet release;	
KM		KM	proliferation; migration; embryogenesis; inflammation; thrombosis;	
KM		KM	geragulation; thrombocytopenia; antibody; thrombotic disorder;	
KM		KM	cerebral vascular disease; stroke; ischaemia; venous thromboembolism;	
KM		KM	leg swelling; pain; ulceration; pulmonary embolism; coronary disease;	
KM		KM	cardiovascular disease; angina pectoris; myocardial infarction;	
KM		KM	coronary restenosis; atherosclerosis; immunological disorder;	
KM		KM	developmental disorder; embryonic disorder; liver disorder;	
KM		KM	cerebral vascular disease; venous thromboembolism disease.	
XX		OS	Homo sapiens.	
XX		PN	MOJC0280368-A1.	
PD		PD	17-OCT-2002.	
XX		P7	09-APR-2002; 2002MO-US11122.	
XX		PR	09-APR-2003; 2003US-0829495.	
XX		XX	(NLL-) MILENNIUM PHARM INC.	
XX		XX	Bussfield SJ, Vileval C, Candrot-Petrus W, Vanherckenck W, Gill CS;	
XX		XX	Olan DW. Kingsbury G.	
XX		XX	WP; 2003-058477/05.	
XX		XX	This invention relates to a novel purified antibody comprising a	
XX		XX	variable heavy (VH) complementarity determined region (CDR1), VH CDR2	
XX		XX	or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3; and	
XX		XX	immunologically binding to a TANGO 268 (also referred as glycoprotein	
XX		XX	VI (GPeVI)) antigen. The antibodies of the invention act to decrease or	
XX		XX	block TANGO 268 binding to extracellular matrix components, or as a	
XX		XX	collagen or platelet release and aggregation blocker. The antibodies of	
XX		XX	disclosure, Page 222-223; 236pp; English.	

CC The invention are useful for modulating proliferation, migration,
 CC morphogeny, differentiation and/or function of megakaryocytes and
 CC platelets, including during development e.g. embryogenesis, modulating
 CC leukocyte-platelet and platelet-endothelium interactions in
 CC inflammation and/or thrombosis, and modulating platelet aggregation and
 CC degradation. They are also useful for modulating disorders associated
 CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
 CC migration, morphology, differentiation and/or function, e.g. bleeding
 CC disorders such as thrombocytopenia. Other diseases which may be
 CC modulated by these antibodies are thrombotic disorders, cerebral
 CC vascular diseases (e.g. stroke and ischaemia), venous thromboembolism
 CC diseases (e.g. diseases involving leg swelling, pain and ulceration),
 CC pulmonary embolism, etc.; coronary diseases (e.g. cardiovascular
 CC diseases including angina pectoris, myocardial infarction, coronary
 CC restenosis, atherosclerosis, etc.); immunological disorders,
 CC developmental disorders, embryonic disorders, liver disorders, cerebral
 CC vascular diseases, venous thromboembolism disease, coronary diseases,
 CC and metastatic cancers. The antibodies of the invention only causes a
 CC transient decrease in platelet counts, platelet aggregation, and/or
 CC platelet activation and so have some advantages over prior art
 CC methods. The present sequence represents a protein sequence used to
 CC create the antibodies of the invention.

XX Sequence 339 AA:

Query Match 99.8%; Score 1782; DB 24; Length 339;
 Best Local Similarity 99.7%; Pred. No. 1,3e-140;
 Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSPSPTALFCLGICLRVPAQSGPLPKRPSQLAPSSJVLPEKVVTLACGSPFVVDLYRLE 60
 DB 1 NSPSPTALFCLGICLRVPAQSGPLPKRPSQLAPSSJVLPEKVVTLACGSPFVVDLYRLE 60
 QY 61 KLSSSRYQCDQAVLFIAMKRSLAGRRCGYQNGSLSPSDQELVATGVFAKPSLSAQP 120
 DB 61 KLSSSRYQCDQAVLFIAMKRSLAGRRCGYQNGSLSPSDQELVATGVFAKPSLSAQP 120
 QY 121 GRAVSSGCVTLCCQCRVGFDFALYKEDFPAPKPKRWKASPHITVTAHSQTRRC 180
 DB 121 GRAVSSGCVTLCCQCRVGFDFALYKEDFPAPKPKRWKASPHITVTAHSQTRRC 180
 QY 181 YGSSRSQPYLWASPDLELVATGTSVTSRLPTFPSSVAEFSATLELTSTNXYFV 240
 DB 181 YGSSRSQPYLWASPDLELVATGTSVTSRLPTFPSSVAEFSATLELTSTNXYFV 240
 QY 241 TTSRSLTTPKESDPPAGPAPQVYTKNLVATCGAVTLLTFLAFLAEDWSPRKQAFH 300
 DB 241 TTSRSLTTPKESDPPAGPAPQVYTKNLVATCGAVTLLTFLAFLAEDWSPRKQAFH 300
 QY 301 RGPAYQRPFLPPLPQCTKSHGCGGCGRQCVHSPGLCS 339
 DB 301 RGPAYQRPFLPPLPQCTKSHGCGGCGRQCVHSPGLCS 339

RESULT 8
 ABU11240
 ID ABU11240 standard; Protein; 339 AA.

XX ABU11240;

XX 06-FEB-2003 (first entry)

DE Glycoprotein VI associated protein sequence #2.

XX Human; mouse; variable heavy; VH; antigen; cancer;
 XX complementarily determining region; RANCO 268; glycoprotein VI; GPIIb;
 XX RANCO 268; extracellular matrix; collagen; platelet release;
 XX proliferation; migration; embryogenesis; inflammation; thrombosis;
 XX degradation; thrombocytopenia; antibody; thrombotic disorders;
 XX cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 XX leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 XX cardiovascular disease; angina pectoris; myocardial infarction;
 XX coronary restenosis; atherosclerosis; immunological disorder;

KX developmental disorder; embryonic disorder; liver disorder;
 KX cerebral vascular disease; venous thromboembolism disease.
 XX Homo sapiens.
 XX NC020263968-A1.
 XX 17-OCT-2002.
 XX 09-APR-2002; 2002MO-JS11122.
 XX 09-APR-2001; 2001US-0829495.
 XX (MILL-) WILKENHUX PHARM INC.
 XX Bristol St. Valleva J. Jandrot-Petrus M. Vainchenker M. Gill DS;
 XX Qian DM, Kingsbury G;
 XX WPI; 2003-058477/05.

XX Novel, substantially purified antibody immunospecifically binding to
 PT RANCO 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
 FT -
 XX Disclosure, Page 223-224; 216pp; English.

XX This invention relates to a novel purified antibody comprising a
 CC variable heavy (VH) complementarily determining region (CDR1, VH CDR2
 CC or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
 CC immunospecifically binding to a RANCO 268 (also referred as glycoprotein
 CC VI (GPIIb)) antigen. The antibodies of the invention act to decrease or
 CC block RANCO 268 binding to extracellular matrix components, or as a
 CC collagen or platelet release and aggregation blocker. The antibodies of
 CC the invention are useful for modulating proliferation, migration,
 CC morphogeny, differentiation and/or function of megakaryocytes and
 CC platelets, including during development e.g. embryogenesis, modulating
 CC leukocyte-platelet and platelet-endothelium interactions in
 CC inflammation and/or thrombosis, and modulating platelet aggregation and
 CC degradation. They are also useful for modulating disorders associated
 CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
 CC migration, morphology, differentiation and/or function, e.g. bleeding
 CC disorders such as thrombocytopenia. Other diseases which may be
 CC modulated by these antibodies are thrombotic disorders, cerebral
 CC vascular diseases (e.g. stroke and ischaemia), venous thromboembolism
 CC diseases (e.g. diseases involving leg swelling, pain and ulceration),
 CC pulmonary embolism, etc.; coronary diseases (e.g. cardiovascular
 CC diseases including angina pectoris, myocardial infarction, coronary
 CC restenosis, atherosclerosis, etc.); immunological disorders,
 CC developmental disorders, embryonic disorders, liver disorders, cerebral
 CC vascular diseases, venous thromboembolism disease, coronary diseases,
 CC and metastatic cancers. The antibodies of the invention only causes a
 CC transient decrease in platelet counts, platelet aggregation, and/or
 CC platelet activation and so have some advantages over prior art
 CC methods. The present sequence represents a protein sequence used to
 CC create the antibodies of the invention.

XX Sequence 339 AA:

Query Match 99.8%; Score 1782; DB 24; Length 339;
 Best Local Similarity 99.7%; Pred. No. 1,3e-140;
 Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSPSPTALFCLGICLRVPAQSGPLPKRPSQLAPSSJVLPEKVVTLACGSPFVVDLYRLE 60
 DB 1 NSPSPTALFCLGICLRVPAQSGPLPKRPSQLAPSSJVLPEKVVTLACGSPFVVDLYRLE 60
 QY 61 KLSSSRYQCDQAVLFIAMKRSLAGRRCGYQNGSLSPSDQELVATGVFAKPSLSAQP 120
 DB 61 KLSSSRYQCDQAVLFIAMKRSLAGRRCGYQNGSLSPSDQELVATGVFAKPSLSAQP 120
 QY 121 GRAVSSGCVTLCCQCRVGFDFALYKEDFPAPKPKRWKASPHITVTAHSQTRRC 180
 DB 121 GRAVSSGCVTLCCQCRVGFDFALYKEDFPAPKPKRWKASPHITVTAHSQTRRC 180

DB 121 GRAVSSGGVLTCCQTRVGFQCFALYKSCDFAPYKNNPERKWRASPIITVTAHSGTYRC 180
 QY 151 YSPSSRDPIYKMSABDPLELVYTGSGVPSRLPTPPSSVMEFSNTALIELVSGFYKVF 240
 DB 161 YSFSSRDPIYKMSABDPLELVYTGSGVPSRLPTPPSSVMEFSNTALIELVSGFYKVF 240
 QY 241 TETSRSTTSPEKSSDPAGAPQYTKKLVICGAVLILLAGFLAEDEWHSRRKRLRH 300
 DB 241 TETSRSTTSPEKSSDPAGAPQYTKKLVICGAVLILLAGFLAEDEWHSRRKRLRH 300
 QY 301 RGRAVQRPPLPPLPQTRKSHGCGGCGRQDVHSGRLCS 339
 DB 301 RGRAVQRPPLPPLPQTRKSHGCGGCGRQDVHSGRLCS 339
 RESULT 9
 ABU11241
 ID ABU11241 standard; Protein: 339 AA.
 AC ABU11241;
 XX
 XX 06-FEB-2003 (first entry)
 DE Glycoprotein VI associated protein sequence #3.
 XX
 XX Human; mouse; variable heavy; VH; antigen: cancer;
 KM complementarity determining region; TANGO 268; glycoprotein VI; GPIV;
 KM TANGO 268; extracellular matrix; collagen; platelet release;
 KM proliferation; migration; embryogenesis; inflammation; thrombosis;
 KM degradation; thrombocytopenia; antibody; thrombotic disorder;
 KM cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KM leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KM cardiovascular disease; angina pectoris; myocardial infarction;
 KM coronary restenosis; atherosclerosis; immunological disorder;
 KM developmental disorder; embryonic disorder; liver disorder;
 KM cerebral vascular disease; venous thromboembolism disease.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO200280968-A1.
 XX
 XX 17-OCT-2002.
 XX
 XX 05-APR-2002; 2002MO-US11122.
 XX
 XX 09-APR-2002; 2002US-08254935.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Busfield SJ, Vileval C, Jandrot-Petruis M, Vainchenker W, Gille DE;
 P1 Qian DX, Kingsbury G;
 P1 WPI: 2003-058477/35.
 DR
 XX
 XX Novel, substantially purified antibody immunospecifically binding to
 P2 TANGO 268 antigen, useful for treating bleeding disorders such as
 P2 thrombocytopenia, stroke, ischaemia, pulmonary embolism, atherosclerosis
 P1
 XX
 XX Disclosure: Page 224-225: 236pp; English.
 XX
 XX This invention relates to a novel purified antibody comprising a
 CC variable heavy (VH) complementarity determining region (CDR1, VH CDR2
 CC or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
 CC immunospecifically binding to a TANGO 268 (also referred as glycoprotein
 CC VI (GPIIb) antigen. The antibodies of the invention act to decrease or
 CC block TANGO 268 binding to extracellular matrix components, or as a
 CC collagen or platelet release and aggregation blocker. The antibodies of
 CC the invention are useful for modulating proliferation, migration,
 CC morphology, differentiation and/or function of megakaryocytes and
 CC platelets, including during development, e.g. embryogenesis, modulating
 CC leukocyte-platelet and platelet-endothelium interactions in
 CC inflammation and/or thrombosis, and modulating platelet aggregation and

CC degradation. They are also useful for modulating disorders associated
 CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
 CC migration, morphology, differentiation and/or function, e.g. bleeding
 CC disorders such as thrombocytopenia. Other diseases which may be
 CC modulated by these antibodies are thrombotic disorders, cerebral
 CC vascular diseases (e.g. stroke and ischaemia) venous thromboembolism
 CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
 CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
 CC diseases including angina pectoris, myocardial infarction, coronary
 CC restenosis, atherosclerosis, etc); immunological disorders,
 CC developmental disorders, embryonic disorders, liver disorders, cerebral
 CC vascular diseases, venous thromboembolism disease, coronary diseases,
 CC and metastatic cancers. The antibodies of the invention only causes a
 CC transient decrease in platelet counts, platelet aggregation, and/or
 CC platelet activation and so have some advantages over prior art
 CC methods. The present sequence represents a protein sequence used to
 CC create the antibodies of the invention.
 XX
 XX Sequence 339 AA:
 SO
 Query Match 99.8%; Score 1782; DB 24; Length 339;
 Best Local Similarity 99.7%; Pired. No. 1,362,403;
 Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YSPSPALPFCGLCLSPVPAQSGPLKPSLQAFSSVLYLEKPVTRCCGPPGVLYRLE 60
 DB 1 MSFSPALPFCGLCLSPVPAQSGPLKPSLQAFSSVLYLEKPVTRCCGPPGVLYRLE 60
 QY 61 KLSSSRVQDAVLFIPAKKSLAGRYRCGYQNGSLMSLESDQLELVATGFAKPSLSAQ 150
 DB 61 KLSSSRVQDAVLFIPAKKSLAGRYRCGYQNGSLMSLESDQLELVATGFAKPSLSAQ 120
 QY 121 GRAVSSGGVLTCCQTRVGFQCFALYKSCDFAPYKNNPERKWRASPIITVTAHSGTYRC 180
 DB 121 GRAVSSGGVLTCCQTRVGFQCFALYKSCDFAPYKNNPERKWRASPIITVTAHSGTYRC 150
 QY 181 YSFSSRDPIYKMSABDPLELVYTGSGVPSRLPTPPSSVMEFSNTALIELVSGFYKVF 240
 DB 181 YSFSSRDPIYKMSABDPLELVYTGSGVPSRLPTPPSSVMEFSNTALIELVSGFYKVF 240
 QY 241 TETSRSTTSPEKSSDPAGAPQYTKKLVICGAVLILLAGFLAEDEWHSRRKRLRH 300
 DB 241 TETSRSTTSPEKSSDPAGAPQYTKKLVICGAVLILLAGFLAEDEWHSRRKRLRH 300
 QY 301 RGRAVQRPPLPPLPQTRKSHGCGGCGRQDVHSGRLCS 339
 DB 301 RGRAVQRPPLPPLPQTRKSHGCGGCGRQDVHSGRLCS 339
 RESULT 10
 ABU11242
 ID ABU11242 standard; Protein: 339 AA.
 AC ABU11242;
 XX
 XX 06-FEB-2003 (first entry)
 DE Glycoprotein VI associated protein sequence #4.
 XX
 XX Human; mouse; variable heavy; VH; antigen: cancer;
 KM complementarity determining region; TANGO 268; glycoprotein VI; GPIV;
 KM TANGO 268; extracellular matrix; collagen; platelet release;
 KM proliferation; migration; embryogenesis; inflammation; thrombosis;
 KM degradation; thrombocytopenia; antibody; thrombotic disorder;
 KM cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KM leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KM cardiovascular disease; angina pectoris; myocardial infarction;
 KM coronary restenosis; atherosclerosis; immunological disorder;
 KM developmental disorder; embryonic disorder; liver disorder;
 KM cerebral vascular disease; venous thromboembolism disease.
 XX
 XX Homo sapiens.

Best Local Similarity 99.1%: Pred. No. 138-139;
Matches 336; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 XSPSPALFCLGCLGAVPAQSGPLPKPSLOALPSSLYLEKVTTLRCQGPFGVDLYRL 60
DQ 1 XSPSPALFCLGCLGAVPAQSGPLPKPSLOALPSSLYLEKVTTLRCQGPFGVDLYRL 60
QY 61 KSSSRVQDQAVLPIPAKMSLAGRVCSYQNGSLMSJSDQJELVA-GVPAKPSLSAQP 120
DQ 61 KSSSRVQDQAVLPIPAKMSLAGRVCSYQNGSLMSJSDQJELVA-GVPAKPSLSAQP 120
QY 121 GPAVSSGGDVTLCCQCRVSGDFALYKESGDPAPYKPERVYKASPTITVAASGTIRC 180
DQ 121 GPAVSSGGDVTLCCQCRVSGDFALYKESGDPAPYKPERVYKASPTITVAASGTIRC 180
QY 181 YSPSSRDPLYMSAPSPLELVITGTSVTPSRLLTPPESSVAEFSSATAEITVAFNKKVFT 240
DQ 181 YSPSSRDPLYMSAPSPLELVITGTSVTPSRLLTPPESSVAEFSSATAEITVAFNKKVFT 240
QY 241 TETSRITTSFKESDSPAGAPQYTKKLVYICGAVYLLIAGFLAEQMSRRKRLRH 300
DQ 241 TETSRITTSFKESDSPAGAPQYTKKLVYICGAVYLLIAGFLAEQMSRRKRLRH 300
QY 301 RGRAVQRPPLPPLPPTCTRKSHGCGGGRQCVHSRGDLS 339
DQ 301 RGRAVQRPPLPPLPPTCTRKSHGCGGGRQCVHSRGDLS 339

RESULT 12
AAV72790 standard; Protein: 339 AA.
ID AAV72790 standard; Protein: 339 AA.
XX AAV72790;
AC AAV72790;
XX 31-MAY-2001 (first entry)
DT 31-MAY-2001 (first entry)
XX Human platelet membrane glycoprotein VI (GPVI).
DE Human platelet membrane glycoprotein VI (GPVI).
XX Human platelet membrane glycoprotein VI; GPVI; thrombolytic therapy;
KW vascular disease; thrombosis.
XX
CS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..23
FT /label= "Signal_peptide"
FT Protein 24..339
FT /note= "Mature platelet membrane glycoprotein VI
FT (GPVI) protein."
FT Domain 24..263
FT /label= "Extracellular_domain"
FT 74
FT Misc-difference /note= "Encoded by TTC"
FT 100
FT Misc-difference /note= "Encoded by AAC"
FT 114
FT Misc-difference /note= "Encoded by CCC"
FT 166
FT Misc-difference /note= "Encoded by CCC"
XX
XX MO2201.6321.AI.
XX PN 38-MAR-2001.
XX PD 01-SEP-2003; 2000MC-US23975.
XX PF 01-SEP-1999; 99US-C152197.
XX PR 08-OCT-1999; 99US-C158251.
XX PA (SUKA) CTSUKA PHAKX CO LTD.
XX PI Tandon N, Sun B, Nakamura T, Yamamoto M;
XX

DR WP1; 2001-226691/23.
DP K-PSDB; AAD02855.
XX
XX Anti-thrombotic medicament, comprising a polypeptide having the
FT extracellular domain of platelet membrane glycoprotein VI or its
FT variant, useful for treating a vascular disease and reducing platelet
FT activation.
XX
XX Disclosure: Fig 3; 74pp; English.
XX
XX The present sequence is a human platelet membrane glycoprotein VI
CC (GPVI). The medicament comprising GPVI is useful for treating
CC vascular disease, and for reducing platelet activation which involves
CC contacting platelets with the medicament. The extracellular portion of
CC GPVI is used therapeutically to attenuate platelet activation and
CC aggregation and to treat thrombosis and other vascular diseases.
CC Anticodices generated against GPVI are used as research and
CC immunotherapeutic agents.
XX
XX Sequence 339 AA;
XX
XX Query Match 98.6%: Score 1759; DB 22; Length 339;
Best Local Similarity 99.1%: Pred. No. 138-139;
Matches 336; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 XSPSPALFCLGCLGAVPAQSGPLPKPSLOALPSSLYLEKVTTLRCQGPFGVDLYRL 60
DQ 1 XSPSPALFCLGCLGAVPAQSGPLPKPSLOALPSSLYLEKVTTLRCQGPFGVDLYRL 60
QY 61 KSSSRVQDQAVLPIPAKMSLAGRVCSYQNGSLMSJSDQJELVA-GVPAKPSLSAQP 120
DQ 61 KSSSRVQDQAVLPIPAKMSLAGRVCSYQNGSLMSJSDQJELVA-GVPAKPSLSAQP 120
QY 121 GPAVSSGGDVTLCCQCRVSGDFALYKESGDPAPYKPERVYKASPTITVAASGTIRC 180
DQ 121 GPAVSSGGDVTLCCQCRVSGDFALYKESGDPAPYKPERVYKASPTITVAASGTIRC 180
QY 181 YSPSSRDPLYMSAPSPLELVITGTSVTPSRLLTPPESSVAEFSSATAEITVAFNKKVFT 240
DQ 181 YSPSSRDPLYMSAPSPLELVITGTSVTPSRLLTPPESSVAEFSSATAEITVAFNKKVFT 240
QY 241 TETSRITTSFKESDSPAGAPQYTKKLVYICGAVYLLIAGFLAEQMSRRKRLRH 300
DQ 241 TETSRITTSFKESDSPAGAPQYTKKLVYICGAVYLLIAGFLAEQMSRRKRLRH 300
QY 301 RGRAVQRPPLPPLPPTCTRKSHGCGGGRQCVHSRGDLS 339
DQ 301 RGRAVQRPPLPPLPPTCTRKSHGCGGGRQCVHSRGDLS 339

RESULT 13
AAB61257
ID AAB61257 standard; Protein: 339 AA.
XX AAB61257;
AC AAB61257;
XX 04-APR-2001 (first entry)
DT 04-APR-2001 (first entry)
XX Mature human TANGO 266 protein.
XX
XX Human; TANGO 266; cardiact; cerebroprotective; cytsstatic; anticoagulant;
KW thrombolytic; antithrombotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
XX Homo sapiens.
XX MO200103810-AI.
XX PN 04-JAN-2001.
XX

PF 30-JUN-2000; 2:50:00-CE18152.
XX
XX 30-JUN-1993; 99US-0345468.
PR 06-DEC-1999; 99US-0454524.
PR 14-FEB-2000; 2000US-0503357.
XX
XX (WILL-) MILLENNIUM PHARM INC.
XX
XX Susfield SJ, Vilella J, Cardrot-Perrus X, Vainchencker W, Gill JS,
PI Qian MD, Kingsbury G.
XX
XX WFI; 2001-080977/09.
XX
XX New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders -
XX
XX Disclosure; Fig 2; 22pp; English.
XX
XX The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI); also called TMCO 258. The GPVI polynucleotide
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
XX
SQ Sequence 319 AA;
Query Match 94.0%; Score 1678; DB 22; Length 319;
Best Local Similarity 100.0%; Pred. No. 6,10-132;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 QSGFLPKPSIQALPSSIVPLEKRPVTLRCGPPGVLDLYREKLSSSRVYQCAVLFPAKRP 60
DB 1 QSGFLPKPSIQALPSSIVPLEKRPVTLRCGPPGVLDLYREKLSSSRVYQCAVLFPAKRP 60
QY 61 SLAGRYRCSYQNGSLWLSLPSDQLELYATGVFAFSLASAGPFAVSSGGVTLQCCRYGF 140
DB 61 SLAGRYRCSYQNGSLWLSLPSDQLELYATGVFAFSLASAGPFAVSSGGVTLQCCRYGF 120
QY 141 DQALYKESHPAFYKPERWRASFPILITVTAHSGTYRCYSSSSDPTLWASDPLEL 200
DB 121 DQALYKESHPAFYKPERWRASFPILITVTAHSGTYRCYSSSSDPTLWASDPLEL 180
QY 201 VWTGTSVTPRLPTPEPSSVAEFSEATLFTVSTKXVPTETSRITTSPPSSSPAP 260
DB 161 VWTGTSVTPRLPTPEPSSVAEFSEATLFTVSTKXVPTETSRITTSPPSSSPAP 240
QY 261 ARGYTKGNLVRLICGAVILITLAGFLAEQMSRRKRLRRGAAVORPLPPLPQTRK 320
DB 241 ARGYTKGNLVRLICGAVILITLAGFLAEQMSRRKRLRRGAAVORPLPPLPQTRK 300
QY 321 SHGGQDGRQDVHSRGLCS 339
DB 301 SHGGQDGRQDVHSRGLCS 319

RESULT 14
AAB49403
ID AAB49403 standard; Protein; 319 AA.
XX
XX AC AAB49403;
XX

QY 35-MAR-2001 (first entry)
XX
XX Human glycoprotein VI mature protein.
XX
XX Human; thrombolytic; cardiac; glycoprotein VI; GPVI;
XX platelet membrane glycoprotein; platelet activation;
XX platelet-collagen interaction; thrombotic disorder;
XX cardiovascular disorder.
XX
XX Homo sapiens.
XX
XX WC00069377-A1.
XX
XX 16-NOV-2000.
XX
XX 25-APR-2000; 2000WO-EP03663.
XX
XX 07-MAY-1999; 99EP-0109094.
XX
XX (MERE) MERCK PATENT GMBH.
XX
XX Clemetson KJ;
XX
XX WPI; 2001-067394/01.
XX
XX N-PSDB: AAC83980.
XX
XX Recombinant human glycoprotein VI, useful for treating thrombotic,
PT cardiovascular diseases or platelet-collagen interactions -
XX
XX Claim 5; Fig 1; 27pp; English.
XX
XX The present sequence is human glycoprotein VI (GPVI) mature protein. GPVI
CC is a platelet membrane glycoprotein which forms a complex together with
CC the heparan common subunit, which is critical for platelet activation in
CC response to collagen. GPVI is useful as a screening tool for detecting
CC specific inhibitors of platelet-collagen interactions, and as a marker
CC for platelet age and platelet exposure to thrombotic and cardiovascular
CC disorders. GPVI is also useful for the manufacture of medicaments in the
CC therapeutic field of thrombotic and cardiovascular events, and disorders
CC related to platelet-collagen interactions.
XX
XX
SQ Sequence 319 AA;
Query Match 94.0%; Score 1675; DB 22; Length 319;
Best Local Similarity 100.0%; Pred. No. 6,10-132;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 QSGFLPKPSIQALPSSIVPLEKRPVTLRCGPPGVLDLYREKLSSSRVYQCAVLFPAKRP 60
DB 1 QSGFLPKPSIQALPSSIVPLEKRPVTLRCGPPGVLDLYREKLSSSRVYQCAVLFPAKRP 60
QY 61 SLAGRYRCSYQNGSLWLSLPSDQLELYATGVFAFSLASAGPFAVSSGGVTLQCCRYGF 140
DB 61 SLAGRYRCSYQNGSLWLSLPSDQLELYATGVFAFSLASAGPFAVSSGGVTLQCCRYGF 120
QY 141 DQALYKESHPAFYKPERWRASFPILITVTAHSGTYRCYSSSSDPTLWASDPLEL 200
DB 121 DQALYKESHPAFYKPERWRASFPILITVTAHSGTYRCYSSSSDPTLWASDPLEL 180
QY 201 VWTGTSVTPRLPTPEPSSVAEFSEATLFTVSTKXVPTETSRITTSPPSSSPAP 260
DB 161 VWTGTSVTPRLPTPEPSSVAEFSEATLFTVSTKXVPTETSRITTSPPSSSPAP 240
QY 261 ARGYTKGNLVRLICGAVILITLAGFLAEQMSRRKRLRRGAAVORPLPPLPQTRK 320
DB 241 ARGYTKGNLVRLICGAVILITLAGFLAEQMSRRKRLRRGAAVORPLPPLPQTRK 300
QY 321 SHGGQDGRQDVHSRGLCS 339
DB 301 SHGGQDGRQDVHSRGLCS 319

RESULT 15

ABU11223
 12 ABU11223 standard; Protein: 319 AA.
 XX
 AC ABU11223;
 XX
 DT 06-FEB-2003 (first entry)
 XX
 LE Human TANGO 268 mature protein.
 XX
 XX Human; mouse; variable heavy; VH; antigen; cancer;
 XX complementarity determining region; TANGO 268; glycoprotein VI; GPII;
 XX TANGO 268; extracellular matrix; collagen; platelet release;
 XX proliferation; migration; embryogenesis; inflammation; thrombosis;
 XX degeneration; thrombocytopenia; antibody; thrombotic disorder;
 XX cerebral; vascular disease; stroke; ischaemia; venous thromboembolism;
 XX leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 XX cardiovascular disease; angina pectoris; myocardial infarction;
 XX coronary restenosis; atherosclerosis; neurological disorder;
 XX developmental disorder; embryonic disorder; liver disorder;
 XX cerebral vascular disease; venous thromboembolism disease.
 XX
 CS Homo sapiens.
 XX
 FN WO200283968-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-US111122.
 XX
 PF 09-APR-2002; 2002WO-US111122.
 XX
 PR 09-APR-2002; 2001US-0829495.
 XX
 PR (MILL.) MILLENNIUM PHARM INC.
 PA
 F1 Busfield SC, Villevall J, Candrol-Perrus M, Vandenacker W, Gill ES;
 F1 Qian JM, Kingsbury G;
 F1
 F1 WPI; 2003-056477/05.
 XX
 XX Novel substantially purified antibody immunospecifically binding to
 F1 TANGO 268 antigen, useful for treating bleeding disorders such as
 F1 thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
 F1
 F1
 PS Disclosure; Page 211-212; 236pp; English.

CC create the antibodies of the invention.
 XX
 S2 Sequence 319 AA;
 Query Match 94.0%; Score 1678; DB 24; Length 319;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-133;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 21 CQGLPRLPLQALPSSLPVLEKPVTLRCGPGGVLYRLEKLSRRYQCAVLFPMKR 80
 1 CQGLPRLPLQALPSSLPVLEKPVTLRCGPGGVLYRLEKLSRRYQCAVLFPMKR 60
 61 SIAGRRRCYQKCSLMSIPSDCLELYATGVFAKPSLSAQGQAVSSGQVTLQCGRYGF 140
 61 SIAGRRRCYQKCSLMSIPSDCLELYATGVFAKPSLSAQGQAVSSGQVTLQCGRYGF 120
 121 DCFALYKEDDPAPYKPEBWRASFPITVTAAHSGTYRQYGFSSRPVMAKSPPLA 200
 121 DCFALYKEDDPAPYKPEBWRASFPITVTAAHSGTYRQYGFSSRPVMAKSPPLA 180
 201 VVTGTSVTPSRPLTEPSSVAEPSEAALITVSFNKVTITTSRSITTSPEGSDPAPG 260
 181 VVTGTSVTPSRPLTEPSSVAEPSEAALITVSFNKVTITTSRSITTSPEGSDPAPG 240
 261 ARGYTKRNLVRIICGAVLCTITAGCLAEQWSPRKRRLHSGRAVGRPLPPLPCLQTRK 320
 241 ARGYTKRNLVRIICGAVLCTITAGCLAEQWSPRKRRLHSGRAVGRPLPPLPCLQTRK 300
 321 SHGGDGGGRQDVHSSRLCS 339
 301 SHGGDGGGRQDVHSSRLCS 319

Search completed: October 23, 2003, 09:41:40
 Job time : 84 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: October 23, 2003, 09:41:49 ; Search time 71 Seconds

Without alignments:
799,566 Million cell updates/sec

Title: US-09-503-387-3

Perfect score: 1796

Sequence: 1 MSPPPALFCLGCLGRVPA.....KSGSGDGGQDVSRSLCS 339

Scoring table: ELOSDM62

Gapop 13.0 , Gapext 3.5

Searched: 629382 seqs, 167460633 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 7

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PC7_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PC7US_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	1786	100.0	339	US-09-832-312-3	Sequence 37, App1
2	1786	100.0	339	US-10-157-031-157	Sequence 397, App1
3	1782	99.8	339	US-09-832-312-34	Sequence 34, App1
4	1782	99.8	339	US-09-832-312-36	Sequence 36, App1
5	1782	99.8	339	US-09-832-312-38	Sequence 38, App1
6	1782	99.8	339	US-09-832-312-40	Sequence 40, App1
7	1759	98.5	339	US-10-446-826-5	Sequence 5, App1
8	1678	94.0	319	US-09-832-312-5	Sequence 5, App1
9	1304	73.0	369	US-10-446-826-17	Sequence 9, App1
10	1122	62.8	313	US-09-832-312-16	Sequence 37, App1
11	1122	62.8	313	US-09-832-312-18	Sequence 18, App1
12	1118	62.6	313	US-09-832-312-42	Sequence 42, App1
13	1118	62.6	313	US-09-832-312-44	Sequence 44, App1
14	1118	62.6	313	US-09-832-312-46	Sequence 46, App1
15	1118	62.6	313	US-09-832-312-46	Sequence 46, App1

16	1080.5	60.5	292	5	US-09-832-312-18	Sequence 18, App1
17	937	52.5	267	9	US-09-832-312-19	Sequence 19, App1
18	498	27.5	447	10	US-09-870-759-50	Sequence 50, App1
19	498	27.9	447	12	US-09-751-708A-50	Sequence 50, App1
20	498	27.9	448	12	US-10-143-6-5-18	Sequence 19, App1
21	498	27.9	448	15	US-10-139-662-18	Sequence 18, App1
22	498	27.5	448	15	US-10-139-662-18	Sequence 18, App1
23	498	27.5	447	11	US-09-978-418-36	Sequence 36, App1
24	477	26.7	289	12	US-10-143-6-18-12	Sequence 12, App1
25	477	26.7	289	15	US-10-139-662-12	Sequence 12, App1
26	457	25.6	432	15	US-10-139-662-12	Sequence 12, App1
27	457	25.6	432	15	US-10-139-662-12	Sequence 12, App1
28	455	25.5	299	11	US-09-756-753-14	Sequence 14, App1
29	455	25.5	293	15	US-10-139-662-10	Sequence 10, App1
30	455	25.5	299	15	US-10-139-662-10	Sequence 10, App1
31	454	25.4	631	9	US-09-832-312-12	Sequence 12, App1
32	449	25.1	631	12	US-10-143-618-20	Sequence 20, App1
33	449	25.1	631	15	US-10-139-662-20	Sequence 20, App1
34	449	25.1	631	15	US-10-139-662-20	Sequence 20, App1
35	441	24.7	466	10	US-09-944-807-12	Sequence 12, App1
36	441	24.7	463	12	US-10-143-618-16	Sequence 16, App1
37	441	24.7	483	15	US-10-139-662-16	Sequence 16, App1
38	441	24.7	483	15	US-10-139-662-16	Sequence 16, App1
39	438.5	24.6	489	12	US-10-143-6-18-14	Sequence 14, App1
40	438.5	24.6	489	15	US-10-139-662-14	Sequence 14, App1
41	438.5	24.6	489	15	US-10-139-662-14	Sequence 14, App1
42	438	24.5	432	15	US-10-290-631-14	Sequence 14, App1
43	438	24.5	432	15	US-10-290-631-14	Sequence 14, App1
44	434	24.3	598	12	US-10-143-6-18-10	Sequence 10, App1
45	434	24.3	598	15	US-10-139-662-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
US-09-832-312-3
Sequence 37, Application US/09832312
Patent No. US20010049829A.
GENERAL INFORMATION:
APPLICANT: Busefield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,119
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,397
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-832-312-3
Query Match 100.0% Score 1796; DB 9; Length 339;
Best Local Similarity 100.0%; Pred No. 2e-135;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 MSPPPALFCLGCLGRVPAAGSGLPEKPELQALPSSLVUEKPVTRCOGPPGVDRYLE 60
DB 1 MSPPPALFCLGCLGRVPAAGSGLPEKPELQALPSSLVUEKPVTRCOGPPGVDRYLE 60
CY 61 KSSSSYQDAVVFPAKRSAGRCYQNGSLWSFSDCLELVATGVFAFPAFSAAP 120
DB 61 KSSSSYQDAVVFPAKRSAGRCYQNGSLWSFSDCLELVATGVFAFPAFSAAP 120

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CY 121 GAAVSSGCVTLCCCTRGVFCQFALYKGGPAPYKQNPFRWYKASFPITTTAAASGTGRC 180
DB 121 GAAVSSGCVTLCCCTRGVFCQFALYKGGPAPYKQNPFRWYKASFPITTTAAASGTGRC 180
CY 181 YFSFSSRDPYKASBPDPLELVYTGTSVPSSEFTFPSSVAFSSATACLTYSNNKVF 240
DB 181 YFSFSSRDPYKASBPDPLELVYTGTSVPSSEFTFPSSVAFSSATACLTYSNNKVF 240
CY 241 TETSRGTTSPKESDSPAQAPARQYVTKGNLVKICGAVILLIAGFLAEDWHSRRKRLRH 300
DB 241 TETSRGTTSPKESDSPAQAPARQYVTKGNLVKICGAVILLIAGFLAEDWHSRRKRLRH 300
CY 301 KRAVQCRPLPLPPLPQCRKSHGGCGGRCQVHSRGLCS 339
DB 301 KRAVQCRPLPLPPLPQCRKSHGGCGGRCQVHSRGLCS 339

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RESULT 2

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US-10-157-031-397
Sequence 387, Application US/10157031
Publication No. US20030108902A1
GENERAL INFORMATION:
APPLICANT: Baranova, A. V.
APPLICANT: Yarkovskiy, N. K.
APPLICANT: Kozlov, A. P.
APPLICANT: Jobashv, A. V.
APPLICANT: Khukovskaya, L. J.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
FILE REFERENCE: 276C-103
CURRENT APPLICATION NUMBER: US/10157031
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 387
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-10-157-031-387

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Query Match 100.0%; Score 1786; DB 15; Length 339;
Best Local Similarity 100.0%; Pred. No. 26-139;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 1 MSPSPALFCLGLCGRVPAQSGPLPKRSJQMLPSSVPLENPTLRCCGPGVDYARLE 60
DB 1 MSPSPALFCLGLCGRVPAQSGPLPKRSJQMLPSSVPLENPTLRCCGPGVDYARLE 60
CY 61 KSSSRVQCAVLFPIPAKRSJAGRYRCSYQNGSLWSJPSQLELVATGVPAKPSLSAQP 120
DB 61 KSSSRVQCAVLFPIPAKRSJAGRYRCSYQNGSLWSJPSQLELVATGVPAKPSLSAQP 120
CY 121 GAAVSSGCVTLCCCTRGVFCQFALYKGGPAPYKQNPFRWYKASFPITTTAAASGTGRC 180
DB 121 GAAVSSGCVTLCCCTRGVFCQFALYKGGPAPYKQNPFRWYKASFPITTTAAASGTGRC 180
CY 181 YFSFSSRDPYKASBPDPLELVYTGTSVPSSEFTFPSSVAFSSATACLTYSNNKVF 240
DB 181 YFSFSSRDPYKASBPDPLELVYTGTSVPSSEFTFPSSVAFSSATACLTYSNNKVF 240
CY 241 TETSRGTTSPKESDSPAQAPARQYVTKGNLVKICGAVILLIAGFLAEDWHSRRKRLRH 300
DB 241 TETSRGTTSPKESDSPAQAPARQYVTKGNLVKICGAVILLIAGFLAEDWHSRRKRLRH 300
CY 301 KRAVQCRPLPLPPLPQCRKSHGGCGGRCQVHSRGLCS 339
DB 301 KRAVQCRPLPLPPLPQCRKSHGGCGGRCQVHSRGLCS 339

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RESULT 3

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US-09-832-312-34
Sequence 34, Application US/09832312
Patent No. US20010049829A1
GENERAL INFORMATION:

```

```

APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,115
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 34
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-832-312-34

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```

Query Match 99.8%; Score 1782; DB 9; Length 339;
Best Local Similarity 99.7%; Pred. No. 4-4e-139;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

CY 1 MSPSPALFCLGLCGRVPAQSGPLPKRSJQMLPSSVPLENPTLRCCGPGVDYARLE 60
DB 1 MSPSPALFCLGLCGRVPAQSGPLPKRSJQMLPSSVPLENPTLRCCGPGVDYARLE 60
CY 61 KSSSRVQCAVLFPIPAKRSJAGRYRCSYQNGSLWSJPSQLELVATGVPAKPSLSAQP 120
DB 61 KSSSRVQCAVLFPIPAKRSJAGRYRCSYQNGSLWSJPSQLELVATGVPAKPSLSAQP 120
CY 121 GAAVSSGCVTLCCCTRGVFCQFALYKGGPAPYKQNPFRWYKASFPITTTAAASGTGRC 180
DB 121 GAAVSSGCVTLCCCTRGVFCQFALYKGGPAPYKQNPFRWYKASFPITTTAAASGTGRC 180
CY 181 YFSFSSRDPYKASBPDPLELVYTGTSVPSSEFTFPSSVAFSSATACLTYSNNKVF 240
DB 181 YFSFSSRDPYKASBPDPLELVYTGTSVPSSEFTFPSSVAFSSATACLTYSNNKVF 240
CY 241 TETSRGTTSPKESDSPAQAPARQYVTKGNLVKICGAVILLIAGFLAEDWHSRRKRLRH 300
DB 241 TETSRGTTSPKESDSPAQAPARQYVTKGNLVKICGAVILLIAGFLAEDWHSRRKRLRH 300
CY 301 KRAVQCRPLPLPPLPQCRKSHGGCGGRCQVHSRGLCS 339
DB 301 KRAVQCRPLPLPPLPQCRKSHGGCGGRCQVHSRGLCS 339

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RESULT 4

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US-09-832-312-36
Sequence 36, Application US/09832312
Patent No. US20010049829A1
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 36
LENGTH: 339
TYPE: PRT

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ORGANISM: Homo sapiens
US-09-832-312-36

Query Match
  Query: 99.8%; Score 1782; DB 9; Length 339;
  Best Local Similarity 99.7%; Pred. No. 4,46-139;
  Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 MSFSTALFCLGICGRVPAQSGPLPKPSLQALPSSLVPLEKPTTLRCQGPVGVLYRLE 60
DB 1 MSPSTALFCLGICGRVPAQSGPLPKPSLQALPSSLVPLEKPTTLRCQGPVGVLYRLE 60
CY 61 KLSRRYQDAVLFITPAKRSACGRYRCYQNGSLMSPLSDOLEVAAGVFAKRSLSAQ 120
DB 61 KLSRRYQDAVLFITPAKRSACGRYRCYQNGSLMSPLSDOLEVAAGVFAKRSLSAQ 120
CY 61 KLSRRYQDAVLFITPAKRSACGRYRCYQNGSLMSPLSDOLEVAAGVFAKRSLSAQ 120
DB 61 KLSRRYQDAVLFITPAKRSACGRYRCYQNGSLMSPLSDOLEVAAGVFAKRSLSAQ 120
CY 121 GPVSSGGDVTLCQCTRYGFDGFALYKGGDPAFYKPERWRASFPITVTAAASGTYRC 180
DB 121 GPVSSGGDVTLCQCTRYGFDGFALYKGGDPAFYKPERWRASFPITVTAAASGTYRC 180
CY 121 GPVSSGGDVTLCQCTRYGFDGFALYKGGDPAFYKPERWRASFPITVTAAASGTYRC 180
DB 121 GPVSSGGDVTLCQCTRYGFDGFALYKGGDPAFYKPERWRASFPITVTAAASGTYRC 180

RESULT 5
US-09-832-312-38
Sequence 38, Application US/09832312
Patient No. US20010043829A1
GENERAL INFORMATION:
  APPLICANT: Busfield et al.
  TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
  FILE REFERENCE: 7853-234
  CURRENT APPLICATION NUMBER: US/09/832,312
  CURRENT FILING DATE: 2001-04-09
  PRIOR APPLICATION NUMBER: 09/610,118
  PRIOR FILING DATE: 2000-06-30
  PRIOR APPLICATION NUMBER: 09/503,387
  PRIOR FILING DATE: 2000-02-14
  PRIOR APPLICATION NUMBER: 09/454,824
  PRIOR FILING DATE: 1999-12-06
  PRIOR APPLICATION NUMBER: 09/345,468
  PRIOR FILING DATE: 1999-06-30
  NUMBER OF SEQ ID NOS: 78
  SOFTWARE: FASTSEQ for Windows Version 3.0
  SEQ ID NO: 38
  TYPE: PRT
  LENGTH: 339
  ORGANISM: Homo sapiens
US-09-832-312-38

Query Match
  Query: 99.8%; Score 1782; DB 9; Length 339;
  Best Local Similarity 99.7%; Pred. No. 4,46-139;
  Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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CY 191 YSFSSRDPLYKMSAPSPLELVITGTSVTPSRCLTTPSSVAEPSEATALLTVSEFYKVF 240
DB 191 YSFSSRDPLYKMSAPSPLELVITGTSVTPSRCLTTPSSVAEPSEATALLTVSEFYKVF 240
CY 241 TETSRSTTSPEKSDSPAGARQYTKGVLRCLGAVLILLAGFLAEDMHSRRRLRH 300
DB 241 TETSRSTTSPEKSDSPAGARQYTKGVLRCLGAVLILLAGFLAEDMHSRRRLRH 300
CY 301 RGRAVQRPPLPPLPQTRKSHSGDGGGRQDVHSRLGS 339
DB 301 RGRAVQRPPLPPLPQTRKSHSGDGGGRQDVHSRLGS 339

RESULT 6
US-09-832-312-40
Sequence 40, Application US/09832312
Patient No. US20010043829A1
GENERAL INFORMATION:
  APPLICANT: Busfield et al.
  TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
  FILE REFERENCE: 7853-234
  CURRENT APPLICATION NUMBER: US/09/832,312
  CURRENT FILING DATE: 2001-04-09
  PRIOR APPLICATION NUMBER: 09/610,118
  PRIOR FILING DATE: 2000-06-30
  PRIOR APPLICATION NUMBER: 09/503,387
  PRIOR FILING DATE: 2000-02-14
  PRIOR APPLICATION NUMBER: 09/454,824
  PRIOR FILING DATE: 1999-12-06
  PRIOR APPLICATION NUMBER: 09/345,468
  PRIOR FILING DATE: 1999-06-30
  NUMBER OF SEQ ID NOS: 78
  SOFTWARE: FASTSEQ for Windows Version 3.0
  SEQ ID NO: 40
  TYPE: PRT
  LENGTH: 339
  ORGANISM: Homo sapiens
US-09-832-312-40

Query Match
  Query: 99.8%; Score 1782; DB 9; Length 339;
  Best Local Similarity 99.7%; Pred. No. 4,46-139;
  Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 MSPSTALFCLGICGRVPAQSGPLPKPSLQALPSSLVPLEKPTTLRCQGPVGVLYRLE 60
DB 1 MSPSTALFCLGICGRVPAQSGPLPKPSLQALPSSLVPLEKPTTLRCQGPVGVLYRLE 60
CY 61 KLSRRYQDAVLFITPAKRSACGRYRCYQNGSLMSPLSDOLEVAAGVFAKRSLSAQ 120
DB 61 KLSRRYQDAVLFITPAKRSACGRYRCYQNGSLMSPLSDOLEVAAGVFAKRSLSAQ 120
CY 121 GPVSSGGDVTLCQCTRYGFDGFALYKGGDPAFYKPERWRASFPITVTAAASGTYRC 180
DB 121 GPVSSGGDVTLCQCTRYGFDGFALYKGGDPAFYKPERWRASFPITVTAAASGTYRC 180
CY 181 YSFSSRDPLYKMSAPSPLELVITGTSVTPSRCLTTPSSVAEPSEATALLTVSEFYKVF 240
DB 181 YSFSSRDPLYKMSAPSPLELVITGTSVTPSRCLTTPSSVAEPSEATALLTVSEFYKVF 240
CY 241 TETSRSTTSPEKSDSPAGARQYTKGVLRCLGAVLILLAGFLAEDMHSRRRLRH 300
DB 241 TETSRSTTSPEKSDSPAGARQYTKGVLRCLGAVLILLAGFLAEDMHSRRRLRH 300
CY 301 RGRAVQRPPLPPLPQTRKSHSGDGGGRQDVHSRLGS 339
DB 301 RGRAVQRPPLPPLPQTRKSHSGDGGGRQDVHSRLGS 339

RESULT 7
US-09-826-5
Sequence 5, Application US/10446826
Publication No. US20030186885A1

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: GENERAL INFORMATION:
: APPLICANT: TANDON, NARENDRA N.
: APPLICANT: SUN, BING
: APPLICANT: NAKAMURA, TAKASHI
: APPLICANT: YAMAWOTO, NAKAMASA
: TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI): DNA AND
: TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
: FILE REFERENCE: 01459.0026-0000
: CURRENT APPLICATION NUMBER: US/10/446,826
: PRIOR FILING DATE: 2003-05-29
: PRIOR APPLICATION NUMBER: US/09/653,2558
: PRIOR FILING DATE: 2003-06-31
: PRIOR APPLICATION NUMBER: PCT/US00/23975
: PRIOR FILING DATE: 2002-09-01
: PRIOR APPLICATION NUMBER: 60/152,197
: PRIOR FILING DATE: 1999-09-01
: PRIOR APPLICATION NUMBER: 60/458,251
: PRIOR FILING DATE: 1999-10-08
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO: 5
: LENGTH: 339
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-503-387-3
:
: Query Match          96.5%; Score 1759; DB 12; Length 339;
: Best Local Similarity 99.1%; Pred. No. 3,5e-137;
: Matches 319; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
:
: Cy 1 NSPSPALFGLICGRVPAGSGPLKPSLICALSSVLEKPVLRCCGPGVDTLYLE 60
: Db 1 NSPSPALFGLICGRVPAGSGPLKPSLICALSSVLEKPVLRCCGPGVDTLYLE 60
:
: Cy 6: KUSSRRYQCAVLEFPAKMSLQAGVPCSYNGSLMSLPDQLELVATGVPAKSLSNQ 120
: Db 6: KUSSRRYQCAVLEFPAKMSLQAGVPCSYNGSLMSLPDQLELVATGVPAKSLSNQ 120
:
: Cy 12: GAVSSGGPVTCCCTRYGFCFALYKECDPAFYKPERWPAASPTITVPAASGTRC 160
: Db 12: GAVSSGGPVTCCCTRYGFCFALYKECDPAFYKPERWPAASPTITVPAASGTRC 160
:
: Cy 18: YFSSRPDYLMASPSPLCVVTGTSVTPSF-PTSPSSVAEFSATLTVSFTNKVFT 240
: Db 18: YFSSRPDYLMASPSPLCVVTGTSVTPSR-PTSPSSVAEFSATLTVSFTNKVFT 240
:
: Cy 241 TTSRSLTSPKSSSPAGPAQVYTKGVNVCAGAVILITLAGEFLADWHSRRLR 300
: Db 241 TTSRSLTSPKSSSPAGPAQVYTKGVNVCAGAVILITLAGEFLADWHSRRLR 300
:
: Cy 30: RGRVGRPLPPLPPTPTKRSKSGGQGVHSGRLS 339
: Db 30: RGRVGRPLPPLPPTPTKRSKSGGQGVHSGRLS 339
:
: US-09-503-387-3
: RESULT 8
: Sequence 5, Application US/09832312
: Patent No. US20010049829A1
: GENERAL INFORMATION:
: APPLICANT: Busfield et al.
: TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
: FILE REFERENCE: 7853-234
: CURRENT APPLICATION NUMBER: US/09/832,312
: PRIOR FILING DATE: 2001-04-09
: PRIOR APPLICATION NUMBER: 09/610,118
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: 09/503,387
: PRIOR FILING DATE: 2000-02-14
: PRIOR APPLICATION NUMBER: 09/454,824
: PRIOR FILING DATE: 1999-12-06
: PRIOR APPLICATION NUMBER: 09/345,468
: PRIOR FILING DATE: 1999-06-30

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: NUMBER OF SEQ ID NOS: 79
: SOFTWARE: FastSeq for Windows Version 1.0
: SEQ ID NO: 5
: LENGTH: 319
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-503-387-3
:
: Query Match          94.0%; Score 1678; DB 9; Length 319;
: Best Local Similarity 100.0%; Pred. No. 1.6e-130;
: Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: Cy 2: QSGPLKPSLICALSSVLEKPVLRCCGPGVDLYRLEKSSRRYQCAVLEFPAK 80
: Db 2: QSGPLKPSLICALSSVLEKPVLRCCGPGVDLYRLEKSSRRYQCAVLEFPAK 80
:
: Cy 31: SLAGRYCSYNGSLMSLPDQLELVATGVPAKPSLSAOPGPAVSGGVDTCCCTRYG 140
: Db 31: SLAGRYCSYNGSLMSLPDQLELVATGVPAKPSLSAOPGPAVSGGVDTCCCTRYG 140
:
: Cy 141 DGFALYKECDPAFYKPERWPAASPTITVPAASGTRC 200
: Db 141 DGFALYKECDPAFYKPERWPAASPTITVPAASGTRC 200
:
: Cy 201 VVTGTSVTPSRPTSPSSVAEFSATLTVSFTNKVFTTSSITSPKSSSPAG 260
: Db 201 VVTGTSVTPSRPTSPSSVAEFSATLTVSFTNKVFTTSSITSPKSSSPAG 260
:
: Cy 261 ARGYTKGNLVRICGAVILITLAGEFLADWHSRRLRHRRVAVRPLPPLPPTK 320
: Db 261 ARGYTKGNLVRICGAVILITLAGEFLADWHSRRLRHRRVAVRPLPPLPPTK 320
:
: Cy 321 SHGGQGVHSGRLS 339
: Db 321 SHGGQGVHSGRLS 339
:
: US-09-503-387-3
: RESULT 9
: Sequence 5, Application US/09832312
: Patent No. US20010049829A1
: GENERAL INFORMATION:
: APPLICANT: Busfield et al.
: TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
: FILE REFERENCE: 7853-234
: CURRENT APPLICATION NUMBER: US/09/832,312
: PRIOR FILING DATE: 2001-04-09
: PRIOR APPLICATION NUMBER: 09/610,118
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: 09/503,387
: PRIOR FILING DATE: 2000-02-14
: PRIOR APPLICATION NUMBER: 09/454,824
: PRIOR FILING DATE: 1999-12-06
: PRIOR APPLICATION NUMBER: 09/345,468
: PRIOR FILING DATE: 1999-06-30
: NUMBER OF SEQ ID NOS: 78
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO: 9
: LENGTH: 249
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-503-387-3
:
: Query Match          73.0%; Score 1304; DB 9; Length 249;
: Best Local Similarity 100.0%; Pred. No. 8.7e-100;
: Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: Cy 21 QSGPLKPSLICALSSVLEKPVLRCCGPGVDLYRLEKSSRRYQCAVLEFPAK 80
: Db 21 QSGPLKPSLICALSSVLEKPVLRCCGPGVDLYRLEKSSRRYQCAVLEFPAK 80
:
: Cy 1 QSGPLKPSLICALSSVLEKPVLRCCGPGVDLYRLEKSSRRYQCAVLEFPAK 60
: Db 1 QSGPLKPSLICALSSVLEKPVLRCCGPGVDLYRLEKSSRRYQCAVLEFPAK 60
:
: Cy 8: SLAGRYCSYNGSLMSLPDQLELVATGVPAKPSLSAOPGPAVSGGVDTCCCTRYG 140

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LENGTH: 313
TYPE: PRT
ORGANISM: Mus musculus
US-09-832-312-48

Query Match 62.6%; Score 1182; DB 9; Length 313;
Best Local Similarity 69.1%; Pred. No. 2,7e-84;
Matches 217; Conservative 25; Mismatches 68; Indels 4; Gaps 2;

QY 1 MSPTALPFCGLGIC-LGRVPAQSGPLPKPSLQALPSSVPLEKPYTLRCQGGPGVCDYRL 59
DB 1 MSPTALPFCGLGIC-LGRVPAQSGPLPKPSLQALPSSVPLEKPYTLRCQGGPGVCDYRL 60
QY 60 EKXSSRPYLMKAPSDPELVYTGCVTPSRLLPTEFSSVAEFSACAEJVSFTNKVF 239
DB 61 EKXKPEKYEEDQDFLF-FTMERSNAGRYRCGYONGSHWS-LPSQLEHLIAGVAKPSLSAH 120
QY 120 PGFAVSSGGDVTLCQCTRYGCFQFALYKEDCPAPYKXNPFKRWYASFP11TVAAHSGTYR 179
DB 121 PSSAVPGGRDVTLCQSPYSFDEFLVYKSGDTGPKYRPEKRWANP11TVAAHSGTYR 180
QY 180 CYFSRSSRPYLMKAPSDPELVYTGCVTPSRLLPTEFSSVAEFSACAEJVSFTNKVF 239
DB 181 CYFSRSSRPYLMKAPSDPELVYTGCVTPSRLLPTEFSSVAEFSACAEJVSFTNKVF 237
QY 240 TTEFSRSITTSPEKSSCPAPAPQVYTKNVLVRCGAVLILLAGFLAEDWHSRKKLR 299
DB 238 TTEKPNVITASPEGLSPFICFAHQHVAKNVLVRCGAVT11LLGLAEDWHSRKKLCQ 297
QY 300 HGRGAVGPPLPPLP 313
DB 298 HRKRALQRPPLPPLP 311

RESULT 13
US-09-832-312-42
Sequence 42; Application US/09812312
Patent No. US20010049829A1
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832-312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 42
TYPE: PRT
ORGANISM: Mus musculus
US-09-832-312-42

Query Match 62.6%; Score 118; DB 9; Length 313;
Best Local Similarity 69.1%; Pred. No. 2,7e-84;
Matches 217; Conservative 25; Mismatches 68; Indels 4; Gaps 2;

QY 1 MSPTALPFCGLGIC-LGRVPAQSGPLPKPSLQALPSSVPLEKPYTLRCQGGPGVCDYRL 59
DB 1 MSPTALPFCGLGIC-LGRVPAQSGPLPKPSLQALPSSVPLEKPYTLRCQGGPGVCDYRL 60
QY 60 EKXSSRPYLMKAPSDPELVYTGCVTPSRLLPTEFSSVAEFSACAEJVSFTNKVF 239
DB 61 EKXKPEKYEEDQDFLF-FTMERSNAGRYRCGYONGSHWS-LPSQLEHLIAGVAKPSLSAH 120
QY 120 PGFAVSSGGDVTLCQCTRYGCFQFALYKEDCPAPYKXNPFKRWYASFP11TVAAHSGTYR 179

DB 121 PSSAVPGGRDVTLCQSPYSFDEFLVYKSGDTGPKYRPEKRWANP11TVAAHSGTYR 180
QY 180 CYFSRSSRPYLMKAPSDPELVYTGCVTPSRLLPTEFSSVAEFSACAEJVSFTNKVF 239
DB 181 CYFSRSSRPYLMKAPSDPELVYTGCVTPSRLLPTEFSSVAEFSACAEJVSFTNKVF 237
QY 240 TTEFSRSITTSPEKSSCPAPAPQVYTKNVLVRCGAVLILLAGFLAEDWHSRKKLR 299
DB 238 TTEKPNVITASPEGLSPFICFAHQHVAKNVLVRCGAVT11LLGLAEDWHSRKKLCQ 297
QY 300 HGRGAVGPPLPPLP 313
DB 298 HRKRALQRPPLPPLP 311

RESULT 14
US-09-832-312-44
Sequence 44; Application US/09812312
Patent No. US20010049829A1
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832-312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
TYPE: PRT
ORGANISM: Mus musculus
US-09-832-312-44

Query Match 62.6%; Score 118; DB 9; Length 313;
Best Local Similarity 69.1%; Pred. No. 2,7e-84;
Matches 217; Conservative 25; Mismatches 68; Indels 4; Gaps 2;

QY 1 MSPTALPFCGLGIC-LGRVPAQSGPLPKPSLQALPSSVPLEKPYTLRCQGGPGVCDYRL 59
DB 1 MSPTALPFCGLGIC-LGRVPAQSGPLPKPSLQALPSSVPLEKPYTLRCQGGPGVCDYRL 60
QY 60 EKXSSRPYLMKAPSDPELVYTGCVTPSRLLPTEFSSVAEFSACAEJVSFTNKVF 239
DB 61 EKXKPEKYEEDQDFLF-FTMERSNAGRYRCGYONGSHWS-LPSQLEHLIAGVAKPSLSAH 120
QY 120 PGFAVSSGGDVTLCQCTRYGCFQFALYKEDCPAPYKXNPFKRWYASFP11TVAAHSGTYR 179
DB 121 PSSAVPGGRDVTLCQSPYSFDEFLVYKSGDTGPKYRPEKRWANP11TVAAHSGTYR 180
QY 180 CYFSRSSRPYLMKAPSDPELVYTGCVTPSRLLPTEFSSVAEFSACAEJVSFTNKVF 239
DB 181 CYFSRSSRPYLMKAPSDPELVYTGCVTPSRLLPTEFSSVAEFSACAEJVSFTNKVF 237
QY 240 TTEFSRSITTSPEKSSCPAPAPQVYTKNVLVRCGAVLILLAGFLAEDWHSRKKLR 299
DB 238 TTEKPNVITASPEGLSPFICFAHQHVAKNVLVRCGAVT11LLGLAEDWHSRKKLCQ 297
QY 300 HGRGAVGPPLPPLP 313
DB 298 HRKRALQRPPLPPLP 311

RESULT 15
US-09-832-312-46

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: Sequence 46, Application US/09032312
: Patent No. US20010049829A1
: GENERAL INFORMATION:
: APPLICANT: Esstfield et al.
: TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
: FILE REFERENCE: 7853-234
: CURRENT APPLICATION NUMBER: US/09/032.312
: CURRENT FILING DATE: 2001-04-09
: PRIOR APPLICATION NUMBER: 09/610.119
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: 09/503.387
: PRIOR FILING DATE: 2000-02-14
: PRIOR APPLICATION NUMBER: 09/454.824
: PRIOR FILING DATE: 1998-12-06
: PRIOR APPLICATION NUMBER: 09/345.468
: PRIOR FILING DATE: 1999-06-30
: NUMBER OF SEQ ID NOS: 78
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 46
: LENGTH: 313
: TYPE: PRT
: ORGANISM: Mus musculus
: US-09-832-312-46

Query Match      62.6%; Score 11.8; DB 9; Length 313;
Best Local Similarity 63.1%; Pred. No. 2,76-84;
Matches 217; Conservative 25; Mismatches 68; Indels 4; Gaps 2;

QY      1 MSPSPPLALFCIGIC-IGRVPAQSGPLPKPSLQAPPSIVFLKPVTLRQGGPPGVLYRQ 53
Db      1 MSPASPFPFCIGVIVIGTQGGPLPKPSLQAPPSIVFLKGVTLRQGGPPGVLYRQ 60
QY      60 EKLSSRRYQDQAVLFTFAKKSLAGRYKSYKNSLWSLPSQDLVLAQVFAKPSLSAQ 119
Db      61 EKLKPEKYEQDPLFTFMERSKAGRYKSYKNSLWSLPSQDLVLAQVFAKPSLSAH 120
QY      120 PGPAVSSGCVTLQCCQTRFGPQDFALYKEGCPAPRYKPEPVYRASFPITVTAAHSGTFR 179
Db      121 PGSAAPGGRDVTAKCSPPSYFDFEVLYKEGCGPYKREKRYRANPPIITVTAAHSGTFR 180
QY      180 CVSFSSRDPPYLWASPSDPLEVVTGTSVTPSRPTPEPPSSVAEFSACAEITVSTTNVF 239
Db      181 CVSFSSSSPYLWASPSDPLVLTGTSATPSSQVPTESFPVTESSRRPSILP---TNKIS 237
QY      240 TTETSRITTSPPKSSSPAPQAPQVYTKGNLVRICGAVILLIAGFLAEQWHSRKRRLR 299
Db      238 TTEKKNITASPEGLSPPGFAHQHYAKGNLVNICGATITILLGLAEQWHSRKRCLQ 297
QY      300 HRCRAVGRPLPPLP 313
Db      296 HMRALGRPLPPLP 311
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Search completed: October 23, 2003, 09:51:23
Run time: 72 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 23, 2003, 11:35:00 ; Search time 20 Seconds

(without alignments)
717.169 Million cell updates/sec

Title: US-09-503-387-3

Perfect score: 1786

Sequence: 1 MSPSTALFGLGLGFPVA.....KSHKQCCGQCVHSRGLCS 339

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310558 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 3%
Maximum Match 100%
Listing first 45 summaries

Database: 1: /cgn2_6/prodata/2/aa/5A_CGMs.pep.*
2: /cgn2_6/prodata/2/aa/5B_CGMs.pep.*
3: /cgn2_6/prodata/2/aa/5A_CGMs.pep.*
4: /cgn2_6/prodata/2/aa/5B_CGMs.pep.*
5: /cgn2_6/prodata/2/aa/PCUTS_CGMs.pep.*
6: /cgn2_6/prodata/2/aa/backfiles.pep.*

Print. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1786	100.0	339	US-09-345-468-3	Sequence 3, Appl1
2	1786	100.0	339	US-09-414-453A-3	Sequence 3, Appl1
3	1786	100.0	339	US-09-832-312-3	Sequence 3, Appl1
4	1782	99.8	339	US-09-832-312-34	Sequence 34, Appl1
5	1782	99.8	339	US-09-832-312-36	Sequence 36, Appl1
6	1782	99.8	339	US-09-832-312-38	Sequence 38, Appl1
7	1782	99.8	339	US-09-832-312-40	Sequence 40, Appl1
8	1678	94.2	319	US-09-345-468-5	Sequence 5, Appl1
9	1678	94.2	319	US-09-414-453A-5	Sequence 5, Appl1
10	1678	94.2	319	US-09-832-312-5	Sequence 5, Appl1
11	1384	73.0	249	US-09-345-468-9	Sequence 9, Appl1
12	1384	73.0	249	US-09-414-453A-9	Sequence 9, Appl1
13	1304	73.0	249	US-09-832-312-9	Sequence 9, Appl1
14	1204	62.8	213	US-09-345-468-6	Sequence 6, Appl1
15	1132	62.8	213	US-09-414-453A-6	Sequence 6, Appl1
16	1132	62.8	213	US-09-832-312-6	Sequence 6, Appl1
17	1132	62.8	213	US-09-832-312-48	Sequence 48, Appl1
18	1118	62.6	213	US-09-832-312-42	Sequence 42, Appl1
19	1118	62.6	213	US-09-832-312-44	Sequence 44, Appl1
20	1118	62.6	213	US-09-832-312-46	Sequence 46, Appl1
21	1080.5	60.5	292	US-09-345-468-16	Sequence 16, Appl1
22	1080.5	60.5	292	US-09-414-453A-16	Sequence 16, Appl1
23	1080.5	60.5	292	US-09-832-312-16	Sequence 16, Appl1
24	937	52.5	267	US-09-345-468-19	Sequence 19, Appl1
25	937	52.5	267	US-09-414-453A-19	Sequence 19, Appl1
26	937	52.5	267	US-09-832-312-19	Sequence 19, Appl1
27	498	27.9	448	US-09-310-463-18	Sequence 18, Appl1

28	498	27.9	448	US-08-842-248A-18	Sequence 18, Appl1
29	477	26.7	289	US-09-310-463-12	Sequence 12, Appl1
30	477	26.7	289	US-08-842-248A-12	Sequence 12, Appl1
31	455	25.5	295	US-09-310-463-30	Sequence 30, Appl1
32	454	25.4	631	US-09-345-468-12	Sequence 12, Appl1
33	454	25.4	631	US-09-414-453A-12	Sequence 12, Appl1
34	454	25.4	631	US-09-832-312-12	Sequence 12, Appl1
35	449	25.1	631	US-09-310-463-20	Sequence 20, Appl1
36	449	25.1	631	US-08-842-248A-20	Sequence 20, Appl1
37	441	24.7	483	US-09-310-463-16	Sequence 16, Appl1
38	441	24.7	483	US-08-842-248A-16	Sequence 16, Appl1
39	438.5	24.6	489	US-09-310-463-14	Sequence 14, Appl1
40	438.5	24.6	489	US-08-842-248A-14	Sequence 14, Appl1
41	438	24.5	431	US-08-985-950-14	Sequence 14, Appl1
42	438	24.5	431	US-08-985-950-20	Sequence 20, Appl1
43	438	24.5	431	US-09-546-049-14	Sequence 14, Appl1
44	438	24.5	431	US-09-546-049-20	Sequence 20, Appl1
45	434	24.3	588	US-09-310-463-10	Sequence 10, Appl1

ALIGNMENTS

RESULT: 1
US-09-345-468-3
Sequence 3, Application US/09345468
Patent No. 624527
GENERAL INFORMATION:
APPLICANT: Busfield, S.
APPLICANT: Vitale, J.
APPLICANT: Jandroc-Petru, M.
APPLICANT: Vancurenker, M.
TITLE OF INVENTION: GYPC PROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-147
CURRENT APPLICATION NUMBER: US/09/345,468
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FASTSEQ for Windows version 3.0
SEQ ID NO 3
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-345-468-3

Query Match 100.0%; Score 1786; DB 3; Length 339;
Best Local Similarity 100.0%; Pred. No. 8,3e+158;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSPSTALFGLGLGRVPAQSGPLPKPSLOALPSLVPLEKPVTLRCGPPGVDPYRL	60
DB	1	MSPSTALFGLGLGRVPAQSGPLPKPSLOALPSLVPLEKPVTLRCGPPGVDPYRL	60
QY	61	KLSRPYODAVLFIFAMKRSLAGRYRCSYONGSLWLSFDLEJYATGVFAKPSISACP	120
DB	61	KLSRPYODAVLFIFAMKRSLAGRYRCSYONGSLWLSFDLEJYATGVFAKPSISACP	120
QY	121	GPVSSGCVETLCCQIRYGFDFALYKEGDPAPYKRPZMYASFTITVTAAHSTYRC	180
DB	121	GPVSSGCVETLCCQIRYGFDFALYKEGDPAPYKRPZMYASFTITVTAAHSTYRC	180
QY	181	YSPSSDPYVMSAPSPLEJYVTGTVTPSR-LTEPPSSVAESEAETELTYSFTYKVT	240
DB	181	YSPSSDPYVMSAPSPLEJYVTGTVTPSR-LTEPPSSVAESEAETELTYSFTYKVT	240
QY	241	TETSRITTSFKESDSFAGPARYCYTKGNLVR-LICAV-LIILAGLADWHSRRPRLSH	300
DB	241	TETSRITTSFKESDSFAGPARYCYTKGNLVR-LICAV-LIILAGLADWHSRRPRLSH	300
QY	301	RGAYAGPAPPLPPLPCTKSHGCGCGCGDYHSRGLCS	339
DB	301	RGAYAGPAPPLPPLPCTKSHGCGCGCGDYHSRGLCS	339

```

RESULT 2
US-09-414-453A-3
; Sequence 3, Application US/0941453A
; Patent No. 538379
; GENERAL INFORMATION:
; APPLICANT: Bostfield, S.
; APPLICANT: Villavai, J.
; APPLICANT: Jandiot-Petrus, M.
; APPLICANT: Vainchenker, M.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT FILING DATE: US/09/414-453A
; PRIOR FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 339
; ORGANISM: Homo sapiens
US-09-414-453A-3

Query Match          100.0%  Score 1766; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 8.3e-158;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MSPPPTALFCGLGCGRVPAQSGPAPKSLQALPSLVLEKPYTLRCQGGPGVLYALE 60
DB 1 MSPPPTALFCGLGCGRVPAQSGPAPKSLQALPSLVLEKPYTLRCQGGPGVLYALE 60
CY 61 KLSSTRYQDAVLEFLPAKRSILAGRYRCSYONGSLMSLPSQCLELVATGVFAKSLSAQP 120
DB 61 KLSSTRYQDAVLEFLPAKRSILAGRYRCSYONGSLMSLPSQCLELVATGVFAKSLSAQP 120
CY 61 KLSSTRYQDAVLEFLPAKRSILAGRYRCSYONGSLMSLPSQCLELVATGVFAKSLSAQP 120
DB 61 KLSSTRYQDAVLEFLPAKRSILAGRYRCSYONGSLMSLPSQCLELVATGVFAKSLSAQP 120
CY 121 GRAVSSGGCVTLCCCTRGVFOGFPALYKSGDPAPYKPRWRASPIITVTAHSGTYRC 180
DB 121 GRAVSSGGCVTLCCCTRGVFOGFPALYKSGDPAPYKPRWRASPIITVTAHSGTYRC 180
CY 121 GRAVSSGGCVTLCCCTRGVFOGFPALYKSGDPAPYKPRWRASPIITVTAHSGTYRC 180
DB 121 GRAVSSGGCVTLCCCTRGVFOGFPALYKSGDPAPYKPRWRASPIITVTAHSGTYRC 180
CY 161 YSFSSRDPEYLMGAPDDELIVYTGTSVTPSRPTEPSSVAEFSSATDELVSFTNKVFT 240
DB 161 YSFSSRDPEYLMGAPDDELIVYTGTSVTPSRPTEPSSVAEFSSATDELVSFTNKVFT 240
CY 241 TETSRITTSPEKESDPAGPARQYTKGNLYRICGAVITLILAGFLAEKHSRKRRLRH 300
DB 241 TETSRITTSPEKESDPAGPARQYTKGNLYRICGAVITLILAGFLAEKHSRKRRLRH 300
CY 301 RGAAGRPPLPPLPQTRKSHSGGSGGGRDGHSGGLCS 339
DB 301 RGAAGRPPLPPLPQTRKSHSGGSGGGRDGHSGGLCS 339

RESULT 3
US-09-832-312-3
; Sequence 3, Application US/09832312
; Patent No. 6548741
; GENERAL INFORMATION:
; APPLICANT: Bostfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT FILING DATE: US/09/832-312
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 339
; ORGANISM: Homo sapiens
US-09-832-312-3

Query Match          99.8%  Score 1782; DB 4; Length 339;
Best Local Similarity 99.7%; Pred. No. 2e-157;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-3

Query Match          100.0%  Score 1766; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 8.3e-158;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MSPPPTALFCGLGCGRVPAQSGPAPKSLQALPSLVLEKPYTLRCQGGPGVLYALE 60
DB 1 MSPPPTALFCGLGCGRVPAQSGPAPKSLQALPSLVLEKPYTLRCQGGPGVLYALE 60
CY 61 KLSSTRYQDAVLEFLPAKRSILAGRYRCSYONGSLMSLPSQCLELVATGVFAKSLSAQP 120
DB 61 KLSSTRYQDAVLEFLPAKRSILAGRYRCSYONGSLMSLPSQCLELVATGVFAKSLSAQP 120
CY 61 KLSSTRYQDAVLEFLPAKRSILAGRYRCSYONGSLMSLPSQCLELVATGVFAKSLSAQP 120
DB 61 KLSSTRYQDAVLEFLPAKRSILAGRYRCSYONGSLMSLPSQCLELVATGVFAKSLSAQP 120
CY 121 GRAVSSGGCVTLCCCTRGVFOGFPALYKSGDPAPYKPRWRASPIITVTAHSGTYRC 180
DB 121 GRAVSSGGCVTLCCCTRGVFOGFPALYKSGDPAPYKPRWRASPIITVTAHSGTYRC 180
CY 161 YSFSSRDPEYLMGAPDDELIVYTGTSVTPSRPTEPSSVAEFSSATDELVSFTNKVFT 240
DB 161 YSFSSRDPEYLMGAPDDELIVYTGTSVTPSRPTEPSSVAEFSSATDELVSFTNKVFT 240
CY 241 TETSRITTSPEKESDPAGPARQYTKGNLYRICGAVITLILAGFLAEKHSRKRRLRH 300
DB 241 TETSRITTSPEKESDPAGPARQYTKGNLYRICGAVITLILAGFLAEKHSRKRRLRH 300
CY 301 RGAAGRPPLPPLPQTRKSHSGGSGGGRDGHSGGLCS 339
DB 301 RGAAGRPPLPPLPQTRKSHSGGSGGGRDGHSGGLCS 339

RESULT 4
US-09-832-312-34
; Sequence 34, Application US/09832312
; Patent No. 6548741
; GENERAL INFORMATION:
; APPLICANT: Bostfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT FILING DATE: US/09/832-312
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; TYPE: PRT
; LENGTH: 339
; ORGANISM: Homo sapiens
US-09-832-312-34

Query Match          99.8%  Score 1782; DB 4; Length 339;
Best Local Similarity 99.7%; Pred. No. 2e-157;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

121 GPAVSSGGDVTLCCQCRVGFDCALYKEDDPAYKXNPERWYASPPILITVPAHSGTYRC 180
181 YSFSSRDPYLMASAPSPLELYVTGTVTSRSLPTPESSVAEFSATDELTVSFTNKVFT 240
182 YSFSSRDPYLMASAPSPLELYVTGTVTSRSLPTPESSVAEFSATDELTVSFTNKVFT 240
241 TETSRSLTTSPEKSDSPAGAPARQYTKGNLVKICGAVILITLIGFLAEDWHSRKRRLR 300
242 TETSRSLTTSPEKSDSPAGAPARQYTKGNLVKICGAVILITLIGFLAEDWHSRKRRLR 300
301 RGRVQRPPLPPLPQTRKSHGQGGQGVHSGGLCS 339
301 RGRVQRPPLPPLPQTRKSHGQGGQGVHSGGLCS 339

```

RESULT 5

```

US-09-832-312-36
Sequence 36, Application US/09832312
Patent No. 6548741
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-832-312-36

```

```

Query Match          99.8%; Score 1782; Dh 4; Length 339;
Best Local Similarity 99.7%; Pred. No. 2e-157;
Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

1 XSPSPALPFLGLGCLGRVPAQSGPLPKSLQALPSSLYVLEKPVTLRCQSPGVLYALE 60
1 XSPSPALPFLGLGCLGRVPAQSGPLPKSLQALPSSLYVLEKPVTLRCQSPGVLYALE 60
61 KSSSRVQDQAVLFIPAKKSLAGRYRCYQNGSLMSLPDLELVATGVSFAKPSLQOF 120
61 KSSSRVQDQAVLFIPAKKSLAGRYRCYQNGSLMSLPDLELVATGVSFAKPSLQOF 120
61 KSSSRVQDQAVLFIPAKKSLAGRYRCYQNGSLMSLPDLELVATGVSFAKPSLQOF 120
121 GPAVSSGGDVTLCCQCRVGFDCALYKEDDPAYKXNPERWYASPPILITVPAHSGTYRC 180
121 GPAVSSGGDVTLCCQCRVGFDCALYKEDDPAYKXNPERWYASPPILITVPAHSGTYRC 180
181 YSFSSRDPYLMASAPSPLELYVTGTVTSRSLPTPESSVAEFSATDELTVSFTNKVFT 240
181 YSFSSRDPYLMASAPSPLELYVTGTVTSRSLPTPESSVAEFSATDELTVSFTNKVFT 240
241 TETSRSLTTSPEKSDSPAGAPARQYTKGNLVKICGAVILITLIGFLAEDWHSRKRRLR 300
241 TETSRSLTTSPEKSDSPAGAPARQYTKGNLVKICGAVILITLIGFLAEDWHSRKRRLR 300
301 RGRVQRPPLPPLPQTRKSHGQGGQGVHSGGLCS 339
301 RGRVQRPPLPPLPQTRKSHGQGGQGVHSGGLCS 339

```

RESULT 6
US-09-832-312-38

```

Sequence 38, Application US/09832312
Patent No. 6548741
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 38
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-832-312-38

```

```

Query Match          99.8%; Score 1782; Dh 4; Length 339;
Best Local Similarity 99.7%; Pred. No. 2e-157;
Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

1 XSPSPALPFLGLGCLGRVPAQSGPLPKSLQALPSSLYVLEKPVTLRCQSPGVLYALE 60
1 XSPSPALPFLGLGCLGRVPAQSGPLPKSLQALPSSLYVLEKPVTLRCQSPGVLYALE 60
61 KSSSRVQDQAVLFIPAKKSLAGRYRCYQNGSLMSLPDLELVATGVSFAKPSLQOF 120
61 KSSSRVQDQAVLFIPAKKSLAGRYRCYQNGSLMSLPDLELVATGVSFAKPSLQOF 120
61 KSSSRVQDQAVLFIPAKKSLAGRYRCYQNGSLMSLPDLELVATGVSFAKPSLQOF 120
121 GPAVSSGGDVTLCCQCRVGFDCALYKEDDPAYKXNPERWYASPPILITVPAHSGTYRC 180
121 GPAVSSGGDVTLCCQCRVGFDCALYKEDDPAYKXNPERWYASPPILITVPAHSGTYRC 180
181 YSFSSRDPYLMASAPSPLELYVTGTVTSRSLPTPESSVAEFSATDELTVSFTNKVFT 240
181 YSFSSRDPYLMASAPSPLELYVTGTVTSRSLPTPESSVAEFSATDELTVSFTNKVFT 240
241 TETSRSLTTSPEKSDSPAGAPARQYTKGNLVKICGAVILITLIGFLAEDWHSRKRRLR 300
241 TETSRSLTTSPEKSDSPAGAPARQYTKGNLVKICGAVILITLIGFLAEDWHSRKRRLR 300
301 RGRVQRPPLPPLPQTRKSHGQGGQGVHSGGLCS 339
301 RGRVQRPPLPPLPQTRKSHGQGGQGVHSGGLCS 339

```

```

RESULT 7
US-09-832-312-40
Sequence 40, Application US/09832312
Patent No. 6548741
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0

```



```

CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: 09/617,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-09-832-312-5

```

```

Query Match          94.0%  Score 1678; DB 4; Length 319;
Best Local Similarity 100.0%  Pred. No. 3e-148;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2: QSGPLPKPSIQALPSSLVPLEKPVTLRCQGPVVDLYRLEKLSSTRYQCAVLFIPAKKR 80
DB 1: QSGPLPKPSIQALPSSLVPLEKPVTLRCQGPVVDLYRLEKLSSTRYQCAVLFIPAKKR 60
QY 8: SLAGRYRCSTYQNSGMSLPSDQLELVATGVFAKPSLSAAGGPAVSSGGCVTLCCQRYGF 140
DB 6: SLAGRYRCSTYQNSGMSLPSDQLELVATGVFAKPSLSAAGGPAVSSGGCVTLCCQRYGF 120
QY 141: DQFALYKEGDPAPYKPERKWRASFPITVTAHSGTYRCYSSSSRDPYLMSAPSDLEL 200
DB 121: DQFALYKEGDPAPYKPERKWRASFPITVTAHSGTYRCYSSSSRDPYLMSAPSDLEL 180
QY 201: VVTGTSVTPSRLLPTEPPSSVAEFSEATAEITVSTFKKVFTEITSRSLTTSRKESDSPAGP 260
DB 181: VVTGTSVTPSRLLPTEPPSSVAEFSEATAEITVSTFKKVFTEITSRSLTTSRKESDSPAGP 240
QY 261: AROYYTKGNLCDAVLTLLAGFLACDWSRKRRLPHERAVORELPPLPOTRK 320
DB 241: AROYYTKGNLCDAVLTLLAGFLACDWSRKRRLPHERAVORELPPLPOTRK 300
QY 321: SHGSGDGGSGQDVHSGIGCS 339
DB 301: SHGSGDGGSGQDVHSGIGCS 319

```

```

RESULT 11
US-09-345-468-9
Sequence 9, Application US/09345468
Patent No. 6245527
GENERAL INFORMATION:
APPLICANT: Busfield, S.
APPLICANT: Villavea, J.
APPLICANT: Candiot-Perrus, M.
APPLICANT: Vainchenker, W.
TITLE OF INVENTION: GLYCOPROTEIN V7 AND USES THEREOF
FILE REFERENCE: 7853-147
CURRENT APPLICATION NUMBER: US/09/345,468
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-345-468-9

```

```

Query Match          73.0%  Score 1394; DB 3; Length 249;
Best Local Similarity 100.0%  Pred. No. 3e-113;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21: QSGPLPKPSIQALPSSLVPLEKPVTLRCQGPVVDLYRLEKLSSTRYQCAVLFIPAKKR 80

```

```

DB 1: QSGPLPKPSIQALPSSLVPLEKPVTLRCQGPVVDLYRLEKLSSTRYQCAVLFIPAKKR 60
QY 81: SLAGRYRCSTYQNSGMSLPSDQLELVATGVFAKPSLSAAGGPAVSSGGCVTLCCQRYGF 140
DB 61: SLAGRYRCSTYQNSGMSLPSDQLELVATGVFAKPSLSAAGGPAVSSGGCVTLCCQRYGF 120
QY 141: DQFALYKEGDPAPYKPERKWRASFPITVTAHSGTYRCYSSSSRDPYLMSAPSDLEL 200
DB 121: DQFALYKEGDPAPYKPERKWRASFPITVTAHSGTYRCYSSSSRDPYLMSAPSDLEL 180
QY 201: VVTGTSVTPSRLLPTEPPSSVAEFSEATAEITVSTFKKVFTEITSRSLTTSRKESDSPAGP 260
DB 181: VVTGTSVTPSRLLPTEPPSSVAEFSEATAEITVSTFKKVFTEITSRSLTTSRKESDSPAGP 240
QY 261: AROYYTKGN 269
DB 241: AROYYTKGN 249

```

```

RESULT 12
US-09-414-453A-9
Sequence 9, Application US/09414453A
Patent No. 6383779
GENERAL INFORMATION:
APPLICANT: Busfield, S.
APPLICANT: Villavea, J.
APPLICANT: Candiot-Perrus, M.
APPLICANT: Vainchenker, W.
TITLE OF INVENTION: GLYCOPROTEIN V7 AND USES THEREOF
FILE REFERENCE: 7853-147
CURRENT APPLICATION NUMBER: US/09/414,453A
CURRENT FILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: US/09/414,453A
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-414-453A-9

```

```

Query Match          73.0%  Score 1394; DB 4; Length 249;
Best Local Similarity 100.0%  Pred. No. 3e-113;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21: QSGPLPKPSIQALPSSLVPLEKPVTLRCQGPVVDLYRLEKLSSTRYQCAVLFIPAKKR 80
DB 1: QSGPLPKPSIQALPSSLVPLEKPVTLRCQGPVVDLYRLEKLSSTRYQCAVLFIPAKKR 60
QY 81: SLAGRYRCSTYQNSGMSLPSDQLELVATGVFAKPSLSAAGGPAVSSGGCVTLCCQRYGF 140
DB 61: SLAGRYRCSTYQNSGMSLPSDQLELVATGVFAKPSLSAAGGPAVSSGGCVTLCCQRYGF 120
QY 141: DQFALYKEGDPAPYKPERKWRASFPITVTAHSGTYRCYSSSSRDPYLMSAPSDLEL 200
DB 121: DQFALYKEGDPAPYKPERKWRASFPITVTAHSGTYRCYSSSSRDPYLMSAPSDLEL 180
QY 201: VVTGTSVTPSRLLPTEPPSSVAEFSEATAEITVSTFKKVFTEITSRSLTTSRKESDSPAGP 260
DB 181: VVTGTSVTPSRLLPTEPPSSVAEFSEATAEITVSTFKKVFTEITSRSLTTSRKESDSPAGP 240
QY 261: AROYYTKGN 269
DB 241: AROYYTKGN 249

```

```

RESULT 13
US-09-832-312-9
Sequence 9, Application US/09832312
Patent No. 6548741
GENERAL INFORMATION:
APPLICANT: Busfield et al.

```

```

1 TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
2 FILE REFERENCE: 7853-234
3 CURRENT APPLICATION NUMBER: US/09/4453A
4 CURRENT FILING DATE: 2001-04-09
5 PRIOR APPLICATION NUMBER: 09/610,116
6 PRIOR FILING DATE: 2000-06-30
7 PRIOR APPLICATION NUMBER: 09/503,387
8 PRIOR FILING DATE: 2000-02-14
9 PRIOR APPLICATION NUMBER: 09/454,824
10 PRIOR FILING DATE: 1999-12-06
11 PRIOR APPLICATION NUMBER: 09/343,468
12 PRIOR FILING DATE: 1999-06-30
13 SOFTWARE: FASTSEQ for Windows Version 3.0
14 SEQ ID NO 9
15 LENGTH: 249
16 TYPE: PRT
17 ORGANISM: Homo sapiens
18 US-09-832-312-9

```

```

Query Match: 73.0%; Score 1364; DB 4; Length 249;
Best Local Similarity: 100.0%; Pred. No. 3e-113;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

CY 21 QSGPLPKPS:QALFSSJVFLEKPTLRQGFPGVD:YRLKX:SSRRYQOAVLFFAMKR 60
DB 1 QSGPLPKPS:QALFSSJVFLEKPTLRQGFPGVD:YRLKX:SSRRYQOAVLFFAMKR 60
CY 61 S.AGRYCSYONGSLMS:PSDQJELVATGVFAKPSLSAOPGAVSSGGVTLQCGTTRGF 140
DB 61 S.AGRYCSYONGSLMS:PSDQJELVATGVFAKPSLSAOPGAVSSGGVTLQCGTTRGF 120
CY 141 DGFALYKGDPAFYKXFERWYRASPFIITVTAHSGTYRCYFSSRDPLYMSAPSDPEL 200
DB 121 DGFALYKGDPAFYKXFERWYRASPFIITVTAHSGTYRCYFSSRDPLYMSAPSDPEL 180
CY 201 VVGTSTVPSKRLTEPPSSVAESEATAEITVSTFKKVTTSRTSRTSPRESPPAGP 260
DB 161 VVGTSTVPSKRLTEPPSSVAESEATAEITVSTFKKVTTSRTSRTSPRESPPAGP 240
CY 261 ARCYVTYKKN 269
DB 241 ARCYVTYKKN 249

```

```

RESULT 14
US-09-345-468-16
1 Sequence 16, Application US/09/4453A
2 Patent No. 6245527
3 GENERAL INFORMATION:
4 APPLICANT: Busfield, S.
5 APPLICANT: Villaveal, J.
6 APPLICANT: Jandrot-Petrus, M.
7 TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
8 FILE REFERENCE: 7853-234
9 CURRENT APPLICATION NUMBER: US/09/345,468
10 CURRENT FILING DATE: 1999-06-30
11 NUMBER OF SEQ ID NOS: 24
12 SOFTWARE: FASTSEQ for Windows Version 3.0
13 SEQ ID NO 16
14 LENGTH: 313
15 TYPE: PRT
16 ORGANISM: Mus musculus
17 US-09-345-468-16

```

```

Query Match: 62.8%; Score 1122; DB 3; Length 313;
Best Local Similarity: 69.4%; Pred. No. 3.3e-96;
Matches 218; Conservative 25; Mismatches 67; Indels 4; Gaps 2;

```

```

CY 1 MSPSPFALFGLG:G-LGRVPAQSGP:FKPSJQALPESLVEKPTLRQGFPGVDLYRL 59
DB 1 MSPSPFALFGLG:G-LGRVPAQSGP:FKPSJQALPESLVEKPTLRQGFPGVDLYRL 60

```

```

CY 60 EKLSSRYQOAVLFFAMKRSLAGRYCSYONGSLMS:PSDQJELVATGVFAKPSLSAOP 119
DB 61 EKLSPKRYEDQPLFIPTHERSNAGRYCSYONGSLMS:PSDQJELVATGVFAKPSLSA 120
CY 120 PGFVASSGGCVTLQCGTTRGFPGDQFALYKGDPAFYKXFERWYRASPFIITVTAHSGTYR 179
DB 121 PGFVAVQGRDVTLKQCSYFSEFVLYKXGDGPYKFEKRYEAFNPFIITVTAHSGTYR 180
CY 180 CYFSSRDPLYMSAPSDPEL:VLTGTSVPSKRLTEPPSSVAESEATAEITVSTFKKVF 239
DB 181 CYFSSRDPLYMSAPSDPEL:VLTGTSVPSKRLTEPPSSVAESEATAEITVSTFKKVF 237
CY 240 TTEKSSITTSFKESDSPAAGPACVYTKNLTWRIC:GAVTLLIAGFLAEDWHRPRKRLR 299
DB 236 TTEKPMKTTASEEGSLPPIGFAHQYAKNLTWRIC:GATVLIITGLLAEQWHRPRKRIQ 297
CY 300 HGRVAVQRPDPPLP 313
DB 298 HGRVAVQRPDPPLP 311

```

```

RESULT 15
US-09-414-453A-16
1 Sequence 16, Application US/09/4453A
2 Patent No. 6383779
3 GENERAL INFORMATION:
4 APPLICANT: Busfield, S.
5 APPLICANT: Villaveal, J.
6 APPLICANT: Jandrot-Petrus, M.
7 TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
8 FILE REFERENCE: 7853-147
9 CURRENT APPLICATION NUMBER: US/09/414,453A
10 CURRENT FILING DATE: 1999-10-07
11 PRIOR APPLICATION NUMBER: 09/345,468
12 PRIOR FILING DATE: 1999-06-30
13 NUMBER OF SEQ ID NOS: 24
14 SOFTWARE: FASTSEQ for Windows Version 3.0
15 SEQ ID NO 16
16 LENGTH: 313
17 TYPE: PRT
18 ORGANISM: Mus musculus
19 US-09-414-453A-16

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Query Match: 62.8%; Score 1122; DB 4; Length 313;
Best Local Similarity: 69.4%; Pred. No. 3.3e-96;
Matches 218; Conservative 25; Mismatches 67; Indels 4; Gaps 2;

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DB 1 MSPSPFALFGLG:G-LGRVPAQSGP:FKPSJQALPESLVEKPTLRQGFPGVDLYRL 60
CY 60 EKLSSRYQOAVLFFAMKRSLAGRYCSYONGSLMS:PSDQJELVATGVFAKPSLSAOP 119
DB 61 EKLSPKRYEDQPLFIPTHERSNAGRYCSYONGSLMS:PSDQJELVATGVFAKPSLSA 120
CY 120 PGFVASSGGCVTLQCGTTRGFPGDQFALYKGDPAFYKXFERWYRASPFIITVTAHSGTYR 179
DB 121 PGFVAVQGRDVTLKQCSYFSEFVLYKXGDGPYKFEKRYEAFNPFIITVTAHSGTYR 180
CY 180 CYFSSRDPLYMSAPSDPEL:VLTGTSVPSKRLTEPPSSVAESEATAEITVSTFKKVF 239
DB 181 CYFSSRDPLYMSAPSDPEL:VLTGTSVPSKRLTEPPSSVAESEATAEITVSTFKKVF 237
CY 240 TTEKSSITTSFKESDSPAAGPACVYTKNLTWRIC:GAVTLLIAGFLAEDWHRPRKRLR 299
DB 236 TTEKPMKTTASEEGSLPPIGFAHQYAKNLTWRIC:GATVLIITGLLAEQWHRPRKRIQ 297
CY 300 HGRVAVQRPDPPLP 313
DB 298 HGRVAVQRPDPPLP 311

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Thu Oct 23 12:03:16 2003

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Search completed: October 23, 2003, 11:38:25
Job time : 21 secs